

; PRIOR APPLICATION NUMBER: US 08/244,924
 ; PRIOR FILING DATE: 1994-11-23
 ; PRIOR APPLICATION NUMBER: US 08/278,644
 ; PRIOR FILING DATE: 1994-07-21
 ; NUMBER OF SEQ ID NOS: 30
 ; SOFTWARE: FASTSEQ for Windows Version 4.0
 ; SEQ ID NO 20
 ; LENGTH: 10
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: p53, 321-330
 ; US-08-452-843A-20

Query Match 57.1% Score 4; DB # Length 10;
 Best Local Similarity 100.0%; Pred. No. 47;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 EYF 6
 Db 6 EYF 9

RESULT 3
 US-10-020-436A-5
 ; Sequence 5; Application US/10020436A
 ; Patent No. US2002015503A1
 ; GENERAL INFORMATION:
 ; APPLICANT: CLARK, JONATHAN
 ; APPLICANT: LAMONT, ALAN
 ; APPLICANT: WILLIAMS, DAVID
 ; TITLE OF INVENTION: A METHOD FOR MAPPING THE ACTIVE SITES BOUND BY ENZYMES
 ; FILE OF INVENTION: THAT COVALENTLY MODIFY SUBSTRATE MOLECULES
 ; FILE REFERENCE: 179-54
 ; CURRENT APPLICATION NUMBER: US/10-020-436A
 ; PRIOR FILING DATE: 2002-05-16
 ; PRIOR APPLICATION NUMBER: 08/278,644
 ; PRIOR FILING DATE: 1994-07-21
 ; PRIOR APPLICATION NUMBER: 08/278,644
 ; PRIOR FILING DATE: 1994-10-30
 ; PRIOR APPLICATION NUMBER: GB 9722818.3
 ; PRIOR FILING DATE: 1997-10-30
 ; NUMBER OF SEQ ID NOS: 19
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 5
 ; LENGTH: 5
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic peptide
 ; US-10-020-436A-5

Query Match 42.9% Score 3; DB # Length 5;
 Best Local Similarity 100.0%; Pred. No. 2.7e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 EYF 5
 Db 3 EYF 5

RESULT 4
 US-10-020-436A-14
 ; Sequence 14; Application US/10020436A
 ; Patent No. US2002015503A1
 ; GENERAL INFORMATION:
 ; APPLICANT: CLARK, JONATHAN
 ; APPLICANT: LAMONT, ALAN
 ; APPLICANT: WILLIAMS, DAVID
 ; TITLE OF INVENTION: A METHOD FOR MAPPING THE ACTIVE SITES BOUND BY ENZYMES
 ; FILE OF INVENTION: THAT COVALENTLY MODIFY SUBSTRATE MOLECULES
 ; FILE REFERENCE: 179-54
 ; CURRENT APPLICATION NUMBER: US/10-020-436A

; CURRENT FILING DATE: 2002-05-16
 ; PRIOR APPLICATION NUMBER: 08/530,431
 ; PRIOR FILING DATE: 2000-07-26
 ; PRIOR APPLICATION NUMBER: PTL 0146, 0019
 ; PRIOR FILING DATE: 1998-10-30
 ; PRIOR APPLICATION NUMBER: GB 9722818.3
 ; PRIOR FILING DATE: 1997-10-30
 ; NUMBER OF SEQ ID NOS: 19
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 14
 ; LENGTH: 5
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic peptide
 ; US-10-020-436A-14

Query Match 42.9% Score 3; DB # Length 5;
 Best Local Similarity 100.0%; Pred. No. 2.7e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 EYF 5
 Db 3 EYF 5

RESULT 5
 US-09-911-129B-13
 ; Sequence 13; Application US/090411129B
 ; Publication No. US20030040600A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Cleveland State University
 ; APPLICANT: Kafatis, Michael
 ; APPLICANT: Mann, Kenneth G.
 ; TITLE OF INVENTION: Tumor Cell Proliferation Inhibitor
 ; FILE REFERENCE: 27433/04004
 ; CURRENT FILING DATE: 2002-03-19
 ; NUMBER OF SEQ ID NOS: 17
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 13
 ; LENGTH: 5
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-09-911-129B-13

Query Match 42.9% Score 3; DB # Length 5;
 Best Local Similarity 100.0%; Pred. No. 2.7e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 EYF 5
 Db 1 EYF 4

RESULT 6
 US-09-859-214-42
 ; Sequence 42; Application US/09850214
 ; Patent No. US2002010311A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Schwender, Charles F.
 ; APPLICANT: Shroff, Hitesh N.
 ; TITLE OF INVENTION: INHIBITORS OF MACCAM-1-MEDIATED
 ; INTERACTIONS AND METHODS OF USE THEREOF
 ; NUMBER OF SEQUENCES: 89
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
 ; STREET: Two Militia Drive
 ; CITY: Lexington
 ; STATE: Massachusetts
 ; COUNTRY: USA
 ; ZIP: 02421
 ; COMPUTER FILEABLE FORM:

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: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/859,214
: FILING DATE: 16-May-2001
: CLASSIFICATION: <Unknown>
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 09/109,874
: FILING DATE: 04-JAN-1996
: APPLICATION NUMBER: US 08/582,740
: FILING DATE: 04-JAN-1996
: ATTORNEY/AGENT INFORMATION:
: NAME: Brook, David E.
: REGISTRATION NUMBER: 22,592
: REFERENCE/DOCKET NUMBER: LKS95-112A
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (781) 861-6240
: TELEFAX: (781) 861-9540
: INFORMATION FOR SEQ ID NO: 42:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 5 amino acids
: TYPE: amino acid
: STRANDEDNESS: <Unknown>
: TOPOLOGY: linear
: MOLECULE TYPE: peptide
: FEATURE:
: NAME/KEY: Modified-site
: LOCATION: 1
: OTHER INFORMATION: /label= modified aa
: /note= "Ac - Leucine"
: FEATURE:
: NAME/KEY: Modified-site
: LOCATION: 5
: OTHER INFORMATION: /label= modified aa
: /note= "Leucine - NH2"
: SEQUENCE DESCRIPTION: SEQ ID NO: 42:
US-09-959-214-42

Query Match 42.9% Score 3; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.7e-05;
Matches 3; Conservative 0; Mismatches 0; Indels 0;

QY 5 FTS 7
DB 2 FTS 4

RESULT 7
US-10-006-630-2
: Sequence 2, Application US/10006630
: Patent No. US20020150926A1
: GENERAL INFORMATION:
: APPLICANT: Jindal, Satish
: APPLICANT: Reulier, Fred
: APPLICANT: Evans, David
: APPLICANT: Williams, Kevin
: APPLICANT: Atiyah, R.
: APPLICANT: Pinali, Aruna
: APPLICANT: Paliwal, Sandeep
: TITLE OF INVENTION: High Speed, automated, continuous flow, multi-dimensional molecular selection and analysis
: FILE REFERENCE: SYP-101DV
: CURRENT APPLICATION NUMBER: US 10-006,630
: PRIOR FILING DATE: 2001-12-05
: PRIOR APPLICATION NUMBER: 09/267,933
: FILING DATE: 1999-03-12
: PRIOR APPLICATION NUMBER: 60/000,518
: PRIOR FILING DATE: 1995-06-26
: PRIOR APPLICATION NUMBER: 09/670,670
: PRIOR FILING DATE: 1996-06-26
: NUMBER OF SEQ ID NOS: 17

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: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 2
: LENGTH: 5
: TYPE: PRT
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: Description of Artificial Sequence: synthetic
: OTHER INFORMATION: peptide
US-10-006-630-2

Query Match 42.9% Score 3; DB 12; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.7e-05;
Matches 3; Conservative 0; Mismatches 0; Indels 0;

QY 3 FTS 5
DB 2 FTS 4

RESULT 8
US-09-727-963A-25
: Sequence 25, Application US/09727963A
: Patent No. US20020155106A1
: GENERAL INFORMATION:
: APPLICANT: V.I. Technologies, Inc.
: APPLICANT: Hammond, David J.
: TITLE OF INVENTION: METHOD FOR IDENTIFYING A LIGAND FOR A TARGET MOLECULE
: FILE REFERENCE: 18242-505
: CURRENT APPLICATION NUMBER: US/09/727,963A
: CURRENT FILING DATE: 2000-12-01
: PRIOR APPLICATION NUMBER: 08/838,658
: PRIOR FILING DATE: 1999-12-02
: NUMBER OF SEQ ID NOS: 99
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 25
: LENGTH: 6
: TYPE: PRT
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: Description of Artificial Sequence: peptide
: OTHER INFORMATION: ligand
US-09-727-963A-25

Query Match 42.9% Score 3; DB 9; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.7e-05;
Matches 3; Conservative 0; Mismatches 0; Indels 0;

QY 4 FTS 6
DB 4 FTS 6

RESULT 9
US-09-895-072-31
: Sequence 31, Application US/0985072
: Patent No. US2002025550A1
: GENERAL INFORMATION:
: APPLICANT: CARFIELD, WILLIAM M
: TITLE OF INVENTION: RETICULATED POLYMERIZING HIGHLY PHOSPHORYLATED LIPIDAL HYDROGELS
: FILE REFERENCE: 2181193SCONT
: CURRENT APPLICATION NUMBER: US/09/895,072
: CURRENT FILING DATE: 2001-07-02
: PRIOR APPLICATION NUMBER: 60/153,831
: PRIOR FILING DATE: 1999-09-14
: PRIOR APPLICATION NUMBER: 09/535,872
: PRIOR FILING DATE: 2000-09-10
: NUMBER OF SEQ ID NOS: 52
: SOFTWARE: PatentIn version 3.1
: SEQ ID NO 31
: LENGTH: 6
: TYPE: PRT
: ORGANISM: Bos taurus
: OTHER INFORMATION: Bos taurus
US-09-895-072-31

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```

OTHER INFORMATION: Artificial Peptide
US-09-839-447A-52
Query Match 42.9% Score 3; DB 10; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.7e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 FTS 7
DB 4 FTS 5

RESULT 10
US-09-476-388-6
Sequence 6, Application US/09876388
Patent No. US20020049159A1
GENERAL INFORMATION:
APPLICANT: Bridon, Dominique P.
APPLICANT: L'Archeveque, Benoit
APPLICANT: Ezrin, Alan M.
APPLICANT: Holmes, Julien L.
APPLICANT: Leblanc, Arouk
APPLICANT: St. Pierre, Serge
TITLE OF INVENTION: LONG LASTING INSULINOMIMETIC PEPTIDES
FILE REFERENCE: 500862001610
CURRENT APPLICATION NUMBER: US-09-074,384
CURRENT FILING DATE: 2001-09-24
PRIOR APPLICATION NUMBER: 08/823,618
PRIOR FILING DATE: 2000-09-05
PRIOR APPLICATION NUMBER: PCT/US00/13563
PRIOR FILING DATE: 2000-05-17
PRIOR APPLICATION NUMBER: 60/159,783
PRIOR FILING DATE: 1999-10-15
PRIOR APPLICATION NUMBER: 60/114,406
PRIOR FILING DATE: 1999-05-17
NUMBER OF SEQ ID NOS: 35
SOFTWARE: Patent in Ver. 2.1
SEQ ID NO 6
LENGTH: 6
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
OTHER INFORMATION: Peptide
US-09-876-388-6

Query Match 42.9% Score 3; DB 10; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.7e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 FTS 7
DB 4 FTS 5

RESULT 11
US-09-839-447A-52
Sequence 52, Application US/09876388
Patent No. US20020049159A1
GENERAL INFORMATION:
APPLICANT: Sallberg, Matti
TITLE OF INVENTION: SYNTHETIC PEPTIDES THAT BIND TO THE
TITLE OF INVENTION: HEPATITIS B VIRUS CORE AND E ANTIGENS
FILE REFERENCE: TPPEP 020GPI
CURRENT APPLICATION NUMBER: US-09/839,447A
CURRENT FILING DATE: 2001-08-09
PRIOR APPLICATION NUMBER: 09/556605
PRIOR FILING DATE: 2000-04-21
NUMBER OF SEQ ID NOS: 111
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 52
LENGTH: 6
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION:

```

```

OTHER INFORMATION: Artificial Peptide
US-09-839-447A-52
Query Match 42.9% Score 3; DB 10; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.7e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 FTS 7
DB 4 FTS 5

RESULT 12
US-09-986-552-31
Sequence 31, Application US/09986552
Patent No. US20020150981A1
GENERAL INFORMATION:
APPLICANT: CANFIELD, William
TITLE OF INVENTION: METHODS FOR PRODUCING HIGHLY PHOSPHORYLATED INSULINAL HYDROLAS
FILE REFERENCE: 2150890S77DIV
CURRENT APPLICATION NUMBER: US-09/986,552
CURRENT FILING DATE: 2001-11-09
PRIOR APPLICATION NUMBER: 09/635,872
PRIOR FILING DATE: 2000-08-10
PRIOR APPLICATION NUMBER: 60/153,831
PRIOR FILING DATE: 1999-09-14
NUMBER OF SEQ ID NOS: 52
SOFTWARE: Patent in version 3.1
SEQ ID NO 31
LENGTH: 6
TYPE: PRT
ORGANISM: Bos taurus
US-09-986-552-31

Query Match 42.9% Score 3; DB 10; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.7e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 FTS 7
DB 3 FTS 5

RESULT 13
US-10-043-487-439
Sequence 439, Application US/10043487
Patent No. US2003035220A1
GENERAL INFORMATION:
APPLICANT: HYBRIGENICS
APPLICANT: Pierre, LEGRAIN
TITLE OF INVENTION: Protein protein interactions between Shigella Flexneri polypep
TITLE OF INVENTION: mammalian polypeptides
FILE REFERENCE: B4778A
CURRENT APPLICATION NUMBER: US-10/043,487
CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US-09/261,130
PRIOR FILING DATE: 2001-01-12
NUMBER OF SEQ ID NOS: 561
SOFTWARE: Patent in version 3.1
SEQ ID NO 439
LENGTH: 7
TYPE: PRT
ORGANISM: Shigella Flexneri
US-10-043-487-439

Query Match 42.9% Score 3; DB 9; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.7e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 YFT 6
DB 3 YFT 5

```

RESULT 14

US-09-056-160B-5

Sequence 5, Application US/09056160B

Patent No. US2002002315A1

GENERAL INFORMATION:

APPLICANT: Baca, Manuel

APPLICANT: Wells, James A.

APPLICANT: Presta, Leonard G.

APPLICANT: Lowman, Henry B.

APPLICANT: Chen, Yvonne M.

TITLE OF INVENTION: ANTI-VEGF ANTI-BODIES

NUMBER OF SEQUENCES: 131

CORRESPONDENCE ADDRESS:

ADDRESSEE: Genentech, Inc.

STREET: 1 DNA Way

CITY: South San Francisco

STATE: California

COUNTRY: USA

ZIP: 94080

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: WinPatIn (Genentech)

CURRENT APPLICATION DATA:

APPLICATION NUMBER US/09-056-160B

FILING DATE: 06-Apr-1998

CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/054,856

FILING DATE: 06-AUG-1997

ATTORNEY/AGENT INFORMATION:

NAME: Hasak, Janet E.

REGISTRATION NUMBER: 28,616

REFERENCE/DOCKET NUMBER: P1093R2

TELECOMMUNICATION INFORMATION:

TELEPHONE: 650/225-1896

TELEFAX: 650/952-9881

INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:

LENGTH: 7 amino acids

TYPE: Amino Acid

TOPOLOGY: Linear

US-09-056-160B-5

Query Match

42.9%, Score 3; DB 10; Length 7;

Best Local Similarity 100.0%; Pred No. 2 7e-05;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 FTS 7

Db 1 FTS 3

RESULT 15

US-09-056-160B-124

Sequence 124, Application US/09056160B

Patent No. US2002002315A1

GENERAL INFORMATION:

APPLICANT: Baca, Manuel

APPLICANT: Wells, James A.

APPLICANT: Presta, Leonard G.

APPLICANT: Lowman, Henry B.

APPLICANT: Chen, Yvonne M.

TITLE OF INVENTION: ANTI-VEGF ANTI-BODIES

NUMBER OF SEQUENCES: 131

CORRESPONDENCE ADDRESS:

ADDRESSEE: Genentech, Inc.

STREET: 1 DNA Way

CITY: South San Francisco

STATE: California

COUNTRY: USA

```

: ZIP: 94080
: COMPUTER READABLE FORM:
: MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: WinPatIn (Genentech)
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09-056-160B
: FILING DATE: 06-Apr-1998
: CLASSIFICATION: 424
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 60/054,856
: FILING DATE: 06-AUG-1997
: ATTORNEY/AGENT INFORMATION:
: NAME: Hasak, Janet E.
: REGISTRATION NUMBER: 28,616
: REFERENCE/DOCKET NUMBER: P1093R2
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 650/225-1896
: TELEFAX: 650/952-9881
: INFORMATION FOR SEQ ID NO: 124:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 7 amino acids
: TYPE: Amino Acid
: TOPOLOGY: Linear
: US-09-056-160B-124

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Query Match

42.9%, Score 3; DB 10; Length 7;

Best Local Similarity 100.0%; Pred. No. 2.7e-05;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 FTS 7

Db 1 FTS 3

Search completed: April 29, 2003, 09:55:22

Job time : 15 secs

GenCore version 5.1.1.LFS-4579
Copyright (c) 1993 - 2003 Computer Ltd

QM protein - protein search, using sw model

Run On: April 29, 2003, 08:45:15 ; Search time 20.8617 seconds
(without alignments)
23,077 million cell updates/sec

Title: US-09-647-749a-1
Perfect score: 5
Sequence: 1 LFSYT 5

Scoring table: Gapped 60 0 0, Gapext 60 0

Searched: 283224 seqs, 96134422 residues

Hit size: 0

Total number of hits satisfying chosen parameters: 1100

Minimum DB seq length: 0
Maximum DB seq length: 10

Post-processing, listing first 45 summaries

2: Pir2:
3: Pir3:
4: Pir4:

Pred No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3	60.0	9	PT0315	Ig heavy chain CRD
2	3	60.0	9	PT0324	Ig heavy chain CRD
3	4	40.0	4	A37912	Phorbol 12-myristate 13-acetate
4	2	40.0	5	I39964	Ribosomal protein
5	2	40.0	5	I39964	Ribosomal protein
6	2	40.0	5	I39965	Ribosomal protein
7	2	40.0	5	I40452	DNAX-like protein
8	2	40.0	5	PT0328	Ig heavy chain CRD
9	2	40.0	5	PT0620	Ig kappa chain V1
10	2	40.0	5	PT0610	T-cell receptor beta
11	2	40.0	5	PT0870	Phytosulfolin kinase
12	2	40.0	6	T11779	Phosphoglycerate kinase
13	2	40.0	6	A31262	Dihydrofolate reductase
14	2	40.0	6	B31262	Dihydrofolate reductase
15	2	40.0	6	T40294	Neuropeptide Y
16	2	40.0	7	1XFYDD	Galactose oxidase
17	2	40.0	7	1NFG7	Hypothalamic hepta
18	2	40.0	7	A60139	Fatty acid synthase
19	2	40.0	7	JN0859	Peptidyl dipeptidase
20	2	40.0	7	T57282	Insulin 57k chain
21	2	40.0	7	T57282	Hypothetical protein
22	2	40.0	7	T57282	Hypothetical protein
23	2	40.0	8	S11078	Glucose-6-phosphat
24	2	40.0	8	T27867	Homeotic protein U
25	2	40.0	8	A28719	Thymic humoral fac
26	2	40.0	8	A61547	Cytochrome P450 AL
27	2	40.0	8	A59028	MHC class I histoc
28	2	40.0	8	A25836	L-serine ammonia-1
29	2	40.0	9	A61357	Phyllocaerulein

30	2	40.0	9	Q24180	Fibrinogen beta ch
31	2	40.0	9	PT0321	Ig heavy chain CRD
32	2	40.0	9	PT0324	Ig heavy chain CRD
33	2	40.0	9	PT0299	Ig heavy chain CRD
34	2	40.0	9	A60427	Macrophage cytotox
35	2	40.0	9	S66635	Alpha-2-macroglobu
36	2	40.0	9	S26509	Collagen alpha 2(V)
37	2	40.0	9	I40416	Cytokeratin 4 - bo
38	2	40.0	9	A28524	Fructose-bisphosph
39	2	40.0	9	PT0443	1-Oxodipicolinate
40	2	40.0	9	S36950	Ig heavy chain V1
41	2	40.0	9	G41946	T-cell receptor ba
42	2	40.0	9	PT0942	T-cell receptor be
43	2	40.0	9	S85802	Hypothetical prote
44	2	40.0	10	1NFG7	Galactosylaminidase
45	2	40.0	10	1NFG7	Galactosylaminidase

ALIGNMENTS

RESULT 1

PT0315
Ig heavy chain CRD3 region (clone 6-109) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 30-Sep-1993 *sequence_revision 30-Sep-1993 *text_change 16-Aug-1994
C:Accession: PT0315
R:Ramaiah, M.; Wasserman, R.; Reichardt, R.A.; Shauer, S.; Cation, A.; Several, S.
J. Exp. Med. 173, 395-407, 1991
A:Title: Preferential utilization of specific immunoglobulin heavy chain diversity an
A:Reference number: PT0315, MIM:1899102, PMID:1899102
A:Accession: PT0315
A:Molecule type: DNA
A:Residues: 1-9 <YAN>
A:Experimental source: B lymphocyte
C:Keywords: heterotetramer; immunoglobulin

Query Match: 60.0%; Score 3; DB 2; Length 9;
Best Local Similarity: 100.0%; Pred. No. 2.8e-05;
Matches: 3; Conservative: 0; Mismatches: 0; Indels: 0

QY 1 LES 3
DB 5 LES 7

RESULT 2

PT0324
Ig heavy chain CRD3 region (clone 6-109) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 30-Sep-1993 *sequence_revision 30-Sep-1993 *text_change 16-Aug-1994
C:Accession: PT0324
R:Ramaiah, M.; Wasserman, R.; Reichardt, R.A.; Shauer, S.; Cation, A.; Several, S.
J. Exp. Med. 173, 395-407, 1991
A:Title: Preferential utilization of specific immunoglobulin heavy chain diversity an
A:Reference number: PT0324, MIM:1899102, PMID:1899102
A:Accession: PT0324
A:Molecule type: DNA
A:Residues: 1-9 <YAN>
A:Experimental source: B lymphocyte
C:Keywords: heterotetramer; immunoglobulin

Query Match: 60.0%; Score 3; DB 2; Length 9;
Best Local Similarity: 100.0%; Pred. No. 2.8e-05;
Matches: 3; Conservative: 0; Mismatches: 0; Indels: 0

QY 2 ESY 4
DB 6 ESY 8

RESULT 3

A37912

phenol 2-monooxygenase (EC 1.14.13.7) chain P5 - Pseudomonas sp. (strain CF600) (fragment)
 C:Species: Pseudomonas sp.
 C:Date: 14-Jun-1991 #sequence_revision 14-Jun-1991 #text_change 23-Jun-1993

C:Accession: A37832
 R:Powlowski, J.; Shingler, V.
 J. Bacteriol. 172, 6834-6840, 1990
 A:Title: In vitro analysis of polypeptide requirements of multicomponent phenol hydroxylase
 A:Reference number: A37832; MUID:91072231; PMID:2274259
 C:Accession: A37832
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-4 <PW>
 C:Keywords: oxidoreductase

Query Match 40.0%; Score 2; DB 2; Length 5;

Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 YT 4

DB 1 SY 2

RESULT 4

139964

ribosomal protein S4 - Bacillus circulans (fragment)

C:Species: Bacillus circulans

C:Date: 19-Jul-1996 #sequence_revision 19-Jul-1996 #text_change 19-Jul-1996

C:Accession: 139964

R:Grundy, F.J.; Henkin, T.M.

J. Bacteriol. 174, 6763-6770, 1992

A:Title: Characterization of the Bacillus subtilis rpsD regulatory target site.

A:Reference number: 139964; MUID:93015735; PMID:1400226

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-5 <RES>

A:Cross-references: GB:M99041; NID:ql43471

C:Genetics:

A:Gene: rpsD

Query Match 40.0%; Score 2; DB 2; Length 5;

Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 YT 5

DB 1 SY 2

RESULT 5

139966

ribosomal protein S4 - Bacillus licheniformis (fragment)

C:Species: Bacillus licheniformis

C:Date: 19-Jul-1996 #sequence_revision 19-Jul-1996 #text_change 19-Jul-1996

C:Accession: 139966

R:Grundy, F.J.; Henkin, T.M.

J. Bacteriol. 174, 6763-6770, 1992

A:Title: Characterization of the Bacillus subtilis rpsD regulatory target site.

A:Reference number: 139966; MUID:93015735; PMID:1400226

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-5 <RES>

A:Cross-references: GB:M99043; NID:ql43475

C:Genetics:

A:Gene: rpsD

Query Match 40.0%; Score 2; DB 2; Length 5;

Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 YT 5

DB 1 SY 2

DB 4 YT 5

RESULT 6

139965

ribosomal protein S4 - Bacillus megaterium (fragment)

C:Species: Bacillus megaterium

C:Date: 19-Jul-1996 #sequence_revision 19-Jul-1996 #text_change 19-Jul-1996

C:Accession: 139965

R:Grundy, F.J.; Henkin, T.M.

J. Bacteriol. 174, 6763-6770, 1992

A:Title: Characterization of the Bacillus subtilis rpsD regulatory target site.

A:Reference number: 139965; MUID:93015735; PMID:1400226

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-5 <RES>

A:Cross-references: GB:M99042; NID:ql43473

C:Genetics:

A:Gene: rpsD

Query Match 40.0%; Score 2; DB 2; Length 5;

Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 YT 5

DB 4 YT 5

RESULT 7

140469

dnazX-like protein - Bacillus subtilis (fragment)

C:Species: Bacillus subtilis

C:Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 21-Jul-1996

C:Accession: 140469

R:Struck, J.C.; Hartmann, R.K.; Toschka, H.Y.; Erdmann, V.A.

Mol. Gen. Genet. 215, 478-482, 1989

A:Title: Transcription and processing of Bacillus subtilis small cytoplasmic RNA.

A:Reference number: 140469; MUID:89218958; PMID:2468993

A:Status: preliminary; translated from DB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-5 <RES>

A:Cross-references: EMBL:X14796; NID:440140; PIDN:CAA32902.1; F01345722.4

C:Genetics:

A:Start codon: GTG

Query Match 40.0%; Score 2; DB 2; Length 5;

Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SY 4

DB 2 SY 3

RESULT 8

PT0308

Ig heavy chain CRD3 region (clone 6-88) - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 11-Aug-1995

C:Accession: PT0308

F:Yamada, M.; Wasserman, P.; Reichard, R.A.; Shane, S.; Caton, A.J.; Kovner, G.

J. Exp. Med. 173, 395-407, 1991

A:Title: Preferential utilization of specific immunoglobulin heavy chain diversity an

A:Reference number: PT0222; MUID:91108337; PMID:1869102

A:Accession: PT0308

A:Molecule type: DNA

A:Residues: 1-5 <YAM>

A:Experimental source: B lymphocyte

C:Keywords: heterotetramer; immunoglobulin

```

Query Match          40.0%; Score 2; DB 3; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ES 3
II
DB 3 ES 4

RESULT 9
JT0520
C:Species: Homo sapiens (man)
C:Date: 23-Oct-1992 #sequence_revision 23-Oct-1992 #text_change 16-Aug-1996
C:Accession: JT0520
R:Anker, R.; Conley, M.F.; Pullak, R.A.
J. Exp. Med. 169, 206-2119, 1989
A:Title: Clonal diversity in the B cell repertoire of patients with X-linked agammaglobulinemia
A:Reference number: JT0511; PMID:85279157; PMID:2336547
Accession: JT0520
Molecule type: mRNA
A:Residues: 1-5 <ANK>
A:Note: The sequence shown here is one of eight productive V-D-J mu chain rearrangements
A:Note: a stop codon terminates the sequence in the V region
C:Keywords: heterotetramer; immunoglobulin
F.1-5/Domain V kappa region <VSE>

Query Match          40.0%; Score 2; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ES 3
II
DB 2 ES 3

RESULT 10
JT0610
C:Species: Mus musculus (house mouse)
C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 10-May-1997
C:Accession: JT0610
R:Peeney, A.T.
J. Exp. Med. 174, 115-124, 1991
A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A:Reference number: JT0509; PMID:41277601; PMID:11559
A:Accession: JT0610
C:Status: translation not shown
Molecule type: mRNA
A:Residues: 1-5 <PEE>
A:Experimental source: newborn thymus, strain BALB/c
C:Keywords: T-cell receptor

Query Match          40.0%; Score 2; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ES 3
II
DB 4 ES 5

RESULT 11
JT0870
C:Species: Asparagus officinalis (garden asparagus)
C:Date: 23-Apr-2002 #sequence_revision 23-Apr-2002 #text_change 19-Apr-2002
C:Accession: JT0870
R:Katsubayashi, Y.; Sakadami, Y.
Proc. Natl. Acad. Sci. U.S.A. 91, 7623-7627, 1994
A:Title: Phytosulfokine, a sulfated peptides that induce the proliferation of single mesophyll cells
A:Reference number: JT0870

Query Match          40.0%; Score 2; DB 3; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ES 3
II
DB 4 ES 5

RESULT 12
JT1779
C:Species: Salmonella typhimurium (fragment)
C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 16-Jul-1999
C:Accession: JT1779
R:Yang, Y.L.; Goldrick, D.; Hong, J.S.
J. Bacteriol. 170, 4299-4303, 1988
A:Title: Identification of the products and nucleotide sequences of two regulatory genes,
A:Reference number: 217239; PMID:8314933; PMID:2842311
A:Accession: JT1779
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-6 <YAN>
A:Cross-references: EMBL:M21279; NID:858752; FID:G151260
A:Experimental source: strain D12

Query Match          40.0%; Score 2; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LE 2
II
DB 2 LE 3

RESULT 13
A31263
C:Species: Plasmodium falciparum
C:Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 20-Mar-1996
C:Accession: A31263
R:Peterson, D.S.; Walliker, D.; Wellem, T.E.
Proc. Natl. Acad. Sci. U.S.A. 95, 9114-9119, 1998
A:Title: Evidence that a point mutation in dihydrofolate reductase-thymidylate synthase
A:Reference number: A94217; PMID:89057886; PMID:2904149
A:Accession: A31263
A:Status: not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-6 <PET>
C:Keywords: methyltransferase; NADP; oxidoreductase

Query Match          40.0%; Score 2; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ES 3
II
DB 4 ES 5

RESULT 14
B31263
C:Species: Plasmodium falciparum
C:Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 20-Mar-1996
C:Accession: B31263
R:Peterson, D.S.; Walliker, D.; Wellem, T.E.
Proc. Natl. Acad. Sci. U.S.A. 95, 9114-9119, 1998
A:Title: Evidence that a point mutation in dihydrofolate reductase-thymidylate synthase

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A:Reference number: A94217; MUID:89057886; PMID:117808

A:Accession: B31263

A>Status: not compared with conceptual translation

A:Molecule type: DNA

A:Residues: 1-6 <PET>

C:Keywords: methyltransferase; NADP; oxidoreductase

Query Match: 40.0%; Score 2; DB 2; Length 6;
Best Local Similarity 100.0%; Pred No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ES 3
II
Db 4 ES 5

RESULT 15

JH0784

Neuropeptide TE-6 - pig roundworm (fragment)

Species: Ascaris suum (pig roundworm)

Date: 10-Jun-1993; #sequence_revision 10; #text_change 28; Apr-1995

C:Accession: JH0784

R:Smart, D.; Shaw, C.; Curry, W.J.; Johnston, C.F.; Thim, L.; Halton, D.W.; Buchanan, K.

Biochem. Biophys. Res. Commun. 187, 1323-1329, 1992

A:Title: The primary structure of TE-6: a novel neuropeptide from the nematode Ascaris

A:Reference number: JH0784; MUID:93048603; PMID:117808

A:Accession: JH0784

A:Molecule type: protein

A:Residues: 1-6 <SMA>

A:Experimental source: gonoduct

C:Keywords: neuropeptide

Query Match: 40.0%; Score 2; DB 2; Length 6;
Best Local Similarity 100.0%; Pred No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LE 2
II
Db 5 LE 6

Search completed: April 29, 2003, 08:54:18

Job time : 22.833 secs

GenCore version 5.1.1 (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: April 29, 2003, 08:30:44 : Search time 11.6667 Seconds
(without alignments)
17.774 Million cell updates/sec

Sequence: 1 LESYT S

Scoring table: OLIGO Gapop 60.0 , Gapext 60.0

Searched: 112892 seqs, 4147628 residues

size: 0
Total number of hits satisfying chosen parameters 346

Minimum DB seq length: 8
Maximum DB seq length: 10

Post-processing: Listing first 45 summaries

Database: SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2	40.0	5	1	PSK_DAUCA
2	2	40.0	7	1	HY7_PIG
3	2	40.0	7	1	IGAD_DACDE
4	2	40.0	8	1	AL16_CARNA
5	2	40.0	8	1	UPAL_HUMAN
6	2	40.0	9	1	PIRB_MAGFU
7	2	40.0	9	1	PIRB_DIAAR
8	2	40.0	9	1	UHA2_HUMAN
9	2	40.0	9	1	ULAH_HUMAN
10	2	40.0	9	1	ULAH_HUMAN
11	2	40.0	9	1	UN19_CLOPA
12	2	40.0	10	1	AMPN_HELAM
13	2	40.0	10	1	CA12_LITCI
14	2	40.0	10	1	CAEP_LITCY
15	2	40.0	10	1	SCN1_ALEMI
16	2	40.0	10	1	SPN1_FERMA
17	2	40.0	10	1	GON3_ONCKE
18	1	20.0	4	1	EGS1_HUMAN
19	1	20.0	4	1	PAR3_HIRME
20	1	20.0	4	1	PAR4_HIRME
21	1	20.0	4	1	FLRF_HIRME
22	1	20.0	4	1	FLRF_HIRME
23	1	20.0	4	1	FLRF_HIRME
24	1	20.0	4	1	FLRF_HIRME
25	1	20.0	4	1	FLRF_HIRME
26	1	20.0	4	1	FLRF_HIRME
27	1	20.0	4	1	FLRF_HIRME
28	1	20.0	4	1	FLRF_HIRME
29	1	20.0	4	1	FLRF_HIRME
30	1	20.0	4	1	FLRF_HIRME
31	1	20.0	4	1	FLRF_HIRME
32	1	20.0	4	1	FLRF_HIRME
33	1	20.0	4	1	FLRF_HIRME

34	1	20.0	5	1	PE31_LITRU
35	1	20.0	5	1	PE32_LITRU
36	1	20.0	5	1	PE33_LITRU
37	1	20.0	5	1	PE34_LITRU
38	1	20.0	5	1	PE35_LITRU
39	1	20.0	5	1	PE36_LITRU
40	1	20.0	5	1	PE37_LITRU
41	1	20.0	5	1	PE38_LITRU
42	1	20.0	5	1	PE39_LITRU
43	1	20.0	5	1	PE40_LITRU
44	1	20.0	5	1	PE41_LITRU
45	1	20.0	5	1	PE42_LITRU

ALIGNMENTS

RESULT 1
PSK_DAUCA
ID PSK_DAUCA STANDARD: PRT: 5 AA.
AC P58261
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Phytosulfokine-alpha (PSK-alpha) [Contains: Phytosulfokine-beta (PSK-beta)]
OS Daucus carota (Carrot)
OC Eukaryota: Viridiplantae: Streptophyta: Embryophyta: Tracheophyta: Spermatophyta: Magnoliophyta: eudicotyledons: core eudicotyledons: Asteridae: euasterids II: Apiales: Apiaceae: Daucus
OX NCBI:taxid:4039
RN [1]
RF SEQUENCE AND IDENTIFICATION BY MASS SPECTROMETRY.
EC STRAIN: 20, HS-Harumakia, Sun
RX MEDLINE: 2012743; PubMed: 10750705
RA Hanai H., Matsuno T., Yamamoto M., Matsubayashi Y., Kobayashi T., Kamada H., Sakagami Y.
RT "A secreted peptide growth factor, phytosulfokine, acting as a stimulatory factor of carrot somatic embryo formation."
EL Plant Cell Physiol 41:27-32(2000)
CC -!- FUNCTION IN PRESENCE OF 1,4- α -SIMULANES PROMOTES DIFFERENTIATION OF THE CELLS, BUT DOES NOT STIMULATE DIFFERENTIATION INTO THE SOMATIC EMBRYOS.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- PTM: SULFATION IS IMPORTANT FOR ACTIVITY AND FOR THE BINDING TO A PUTATIVE MEMBRANE RECEPTOR (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE PHYTOSULFOKINE FAMILY.
KW Growth factor; Sulfation.
FT PEPTIDE 1 4 PHYTOSULFOKINE-RETA.
FT MOD_RES 1 1 SULFATION.
FT MOD_RES 3 3 SULFATION.
SQ SEQUENCE 5 AA: 687 MW; 7601BB504B300000 CRC64:

Query Match
Best Local Similarity: 100.0%, P-Val: 1.1e-05; Length: 5
Matches: 2, Coverage: 40%, Mismatches: 0, Gaps: 0

QY 4 YI 5
DB 3 YI 4

RESULT 2

HY7_PIG
ID HY7_PIG STANDARD: PRT: 7 AA.
AC P01153
DT 21-JUL-1986 (Rel. 01, Created)
DT 31-JUL-1986 (Rel. 01, Last annotation update)
DE Hypothalamic heptapeptide.
OS Sus scrofa (Pig)
OC Eukaryota: Metazoa: Chordata: Cladocera: Vertebrata: Euteleostomi: Mammalia: Eutheria: Cetartiodactyla: Suina: Suidae: Sus

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ON NCBI_TaxID=9823;
RX [1]
RP SEQUENCE, AND SYNTHESIS.
RX MEDLINE=81213950; PubMed=6263776;
PA Chang P C C., Huang W Y., Arimura A., Redding T W., Coy D H.,
FA Saifan M., Kong A., Hamilton J W., Goh D V., Schally A V.,
RT "Isolation, structure and synthesis of a heptapeptide with in vitro
RT ACTH-releasing activity from porcine hypothalamus.";
RL Horm. Metab. Res. 13:228-232(1981);
DR PIR: A01417; NYP67.
SQ SEQUENCE 7 AA: 957 MW: 632545b1e5b5c2a0 CRC64;

Query Match 40.0%; Score 2; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SY 4
DB 5 SY 6

RESULT 3
ID IGAO_DACDE STANDARD; PRI: 7 AA.
AC P06294;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 01-OCT-1994 (Rel. 30, Last annotation update)
DE Galactose oxidase inhibitor.
OS Dactylium dendroides (Cladobotryum dendroides).
OC Eukaryota, Fungi, Ascomycota, Pezizomycotina, Sordariomycetes;
OC Hypocreales; Hypocreaceae; Hypomyces.
OX NCBI_TaxID=5132;
RN [1]
RP SEQUENCE.
RA Avigad G., Markus 2.1.
RT "Identification of a peptide inhibitor of galactose oxidase from
RT Dactylium dendroides."
RL Fed. Proc. 31:447-447(1972).
CC -!- FUNCTION: BINDS ONE COPPER ION PER MOLECULE BUT DOES NOT BIND THE
CC GALACTOSE OXIDASE APOENZYME. IT MAY INACTIVATE THE ENZYME BY
CC BINDING TO ITS PROSTHETIC COPPER GROUP
DR PIR: A01341; XEYDGD.
KW Copper, Metalloenzyme inhibitor.
SQ SEQUENCE 7 AA: 706 MW: 75BB01A456D87D80 CRC64;

Query Match 40.0%; Score 2; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0.

QY 2 ES 3
DB 6 ES 7

RESULT 4
ID ALL6_CARMA STANDARD; PRI: 8 AA.
AC P81819;
DT 30-MAY-2000 (Rel. 14, Created)
DT 30-MAY-2000 (Rel. 14, Last sequence update)
DT 30-MAY-2000 (Rel. 14, Last annotation update)
DE Carcinustatin 16.
OS Carcinus maenas (Common shore crab) (Green Crab).
OC Eukaryota; Metazoa; Arthropoda, Mandibulata, Furcunculata, Crustacea;
OC Malacostraca; Eumalacostraca; Eucarida; Decapoda; Pleocyemata;
OC Brachyura; Eubrachyura; Portunoidae; Portunidae; Carcinus.
OX NCBI_TaxID=6759;
RN [1]
RP SEQUENCE.
RA Duve H., Cohnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,

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RA Thorpe A.;
RT "Isolation and identification of multiple neuropeptides of the
RT allatostatin superfamily in the shore crab Carcinus maenas.";
RL Eur. J. Biochem. 250:757-774(1997).
CC -!- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR.
CC -!- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
KW Neuropeptide; Amidation; Multigene family.
FT MOD_RES 8 AMIDATION.
SV SEQUENCE 8 AA: 613 MW: 73286545A576878 CRC64;

Query Match 40.0%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SY 4
DB 5 SY 6

RESULT 5
ID UPAL_HUMAN STANDARD; PRI: 8 AA.
AC P30087;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Unknown protein from CD-page of plasma (Spot 2) (Fragment).
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini, Hominiidae, Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RC TISSUE=Plasma;
RX MEDLINE=9309293; PubMed=1459097;
RA Hughes G.C., Frutiger S., Faquet N., Ravier F., Pasquali C.,
FA Sanchez J.-C., James P., Tissot J.-D., Bjellqvist B.,
RA Hochstrasser D.F.;
RT "Plasma protein map: an update by microsequencing."
RL Electrophoresis 13:707-714(1992).
CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC PROTEIN IS: 4.9, ITS MW IS: 65 KDa
DR SWISS-2DPAGE; P30087; HUMAN.
FT NON_TER 1
FT UNSURE 8
FT NON_TER 8
SV SEQUENCE 8 AA: 944 MW: C01772455BB06DA CRC64;

Query Match 40.0%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ES 3
DB 3 ES 4

RESULT 6
ID FIBB_MAFU STANDARD; PRI: 9 AA.
AC P19345;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Fibrinogen beta chain (Contains: Fibrinopeptide B) (Fragment).
OS Macaca fuscata fuscata (Japanese macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;
OC Cercopitheciae; Macaca.
OX NCBI_TaxID=9543;
RN [1]
RP SEQUENCE.

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RX MEDLINE=85289140; PubMed=3928610;
 RA Nakamura S, Takenaka O, Takahashi K;
 RT "Fibrinopeptides A and B of Japanese monkey (*Macaca fuscata*) and
 RT pates monkey (*Erythrocebus patas*): their amino acid sequences,
 RT restricted mutations, and a molecular phylogeny for macaques,
 RT quonons, and baboons";
 RL J. Biochem. 97:1487-1492(1985).
 CC -1- FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT
 CC POLYMERIZE INTO FIBRIN AND ACTING AS A CLOT FACTOR IN PLATELET
 CC AGGREGATION.
 CC -1- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NON-IDENTICAL CHAINS
 CC (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
 CC -1- MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY
 CC THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA
 CC CHAINS, AND THIS EXPOSES THE N-TERMINAL POLYMERIZATION SITES
 CC RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT.
 DR PIR: C24190; C21180.
 DR Interpro: IPR00181; Fibrinogen_C.
 DR PROSITE: PS00514; FIBRIN_AG_C_DOMAIN: PARTIAL
 R Blood coagulation: Plasma.
 P PEPTIDE 1 9 FIBRINOPEPTIDE B
 NON_TER 1 9
 SQ SEQUENCE 9 AA: 1038 MW: 69F65B9C735B81P APC64:
 Query Match 40.0% Score 2: DB 1: Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.1e+05;
 Matches 2: Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 ES 3
 DB 3 ES 4
 RESULT 7
 PGLR_DIAAB STANDARD: PRT: 9 AA.
 ID PGLR_DIAAB
 AC P81179;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Endo-polygalacturonase (PG) (EC 3.2.1.15) (Fragment).
 OS Diaprepes abbreviatus (Superficial root-knot-disease-transmitting
 OS Eukaryota; Metazoa; Arthropoda; Mandibulata; Insecta; Hexapoda;
 Insecta; Pterygota; Neoptera; Endopterygota; Coleoptera; Polyphaga;
 Cucujiformia; Phytophaga; Curculionidae; Entiminae; Entimini;
 Diaprepes
 CC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE.
 TISSUE=Larval gut;
 RA Doostdar H., McCollum T.G., Mayer R.T.;
 RT "Purification and characterization of an endo-polygalacturonase from
 RT the gut of West Indian sugarcane root-knot-transmitting Diaprepes
 RT abbreviatus L. larvae";
 RL Comp. Biochem. Physiol. 118B:861-867(1987).
 CC -1- CATALYTIC ACTIVITY: Random hydrolysis of 1,4-alpha-D-
 CC galactosiduronic linkages in pectate and other galacturonans.
 CC -1- INDUCTION: INHIBITED BY CITRUS PGIP.
 CC -1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS PROTEIN IS:
 CC 9.4, ITS MW IS: 44.5 kDa
 CC -1- SIMILARITY: WEAK TO OTHER POLYGALACTURONASES.
 KW Hydrolase; Glycosidase; Cell wall.
 FT NON_TER 9
 SQ SEQUENCE 9 AA: 1041 MW: 1F49087042D841P APC64:
 Query Match 40.0% Score 2: DB 1: Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.1e+05;
 Matches 2: Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 4 YT 5
 DB 2 YT 3

RESULT 8
 UHA2_HUMAN STANDARD: PRT: 9 AA.
 ID UHA2_HUMAN
 AC P40920;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 15-OCT-2001 (Rel. 40, Last annotation update)
 LE Unknown protein from 2D-page of heart (Spot 5003) (Fragment).
 OS Homo sapiens (Human).
 CC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE.
 TISSUE=Heart;
 RX MEDLINE=91203297; PubMed=7895232;
 RA Corbett J.M., Wheeler C.H., Baker C.S., Yacoub M.H., Dunn M.C.;
 RT "The human myocardial two-dimensional gel protein database: update
 RT 1994.";
 RL Electrophoresis 15:1459-1465(1994).
 CC -1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKN KN
 CC PROTEIN IS: 6.0, ITS MW IS: 55.3 kDa.
 FT NON_TER 9
 SQ SEQUENCE 9 AA: 1104 MW: 8874B1B5B01B2CA CRC64:
 Query Match 40.0% Score 2: DB 1: Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.1e+05;
 Matches 2: Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 4 YT 5
 DB 6 YT 7
 RESULT 9
 ULAE_HUMAN STANDARD: PRT: 9 AA.
 ID ULAE_HUMAN
 AC P31931;
 DT 01-JUL-1993 (Rel. 26, Created)
 DT 01-JUL-1993 (Rel. 26, Last sequence update)
 DE Liver 2001 (Fet. 48, Last annotation update)
 DE Unknown protein from 2D-page of liver tissue (Spot 110) (Fragment).
 OS Homo sapiens (Human).
 CC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE.
 TISSUE=Liver;
 RX MEDLINE=94147969; PubMed=8313870;
 RA Hughes G.J., Frutiger S., Paquet N., Pasquali C., Sanchez J.-C.,
 RA Tissot F.D., Baerich A., Appel S.D., Hochstrasser D.F.;
 RT "Human liver protein map: update 1993.";
 RL Electrophoresis 14:1216-1224(1993).
 CC -1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKN KN
 CC PROTEIN IS: 5.5, ITS MW IS: 11 kDa.
 DR SWISS-2DPAGE; P31931; HUMAN.
 FT NON_TER 9
 SQ SEQUENCE 9 AA: 1096 MW: 477B3B173AE729C7 CRC64:
 Query Match 40.0% Score 2: DB 1: Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.1e+05;
 Matches 2: Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LE 2
 DB 6 LE 7
 RESULT 10
 ULAH_HUMAN STANDARD: PRT: 9 AA.
 ID ULAH_HUMAN

CC -1- TISSUE SPECIFICITY: SECRETED BY THE SKIN DORSAL GLANDS.
 CC -1- PFM: IS-POPM 1 2Y4 DIFFERS FROM IS-PE-PM 1 2 IN NMI BEING
 CC SULFATED.

CC -1- MASS SPECTROMETRY: MW=1356; METHOD=Electro-spray.

CC -1- SIMILARITY: BELONGS TO THE GASTRIN/CHOLESTYKININ FAMILY

DR InterPro: IPR001651; Gastrin.

DR PROSITE: PS00259; Gastrin.

DR Amphibian skin: Hypotensive agent: Amidation. Sulfation.

FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.

FT MOD_RES 4 4 SULFATION.

FT MOD_RES 10 10 AMIDATION.

FT MOD_RES 10 10 AMIDATION.

SQ SEQUENCE 10 AA: 1306 MW: 9905637861864A CRC64:

Query Match 40.0%; Score 2; DB 1; Length 10;

Best Local Similarity 100.0%; Pred. No. 4.3e+03;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 YT 5

DB 4 YT 5

RESULT 14

CAER_LITXA STANDARD: PRT: 10 AA.
 AC P56264;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Caerulein.

US Litoria xanthomera (Orange-thighed frog).

CC Eukaryota; Chordata; Vertebrata; Euteleostomi;

CC Amphibia; Batrachia; Anura; Neobatrachia; Bufonidae; Hylidae;

CC Pelodyadinae; Litoria.

OX NCBI_TaxID=79697;

RN [1]

RP SEQUENCE, AND MASS SPECTROMETRY.

PC TISSUE-Skin secretion;

RX MEDLINE=97374000; PubMed=9230483;

RA Steinboerner S T, Waugh R J, Rowie J H, Wallace J C, Tyler M J,

Ramsay S L;

RT "New caerin antibacterial peptides from the skin glands of the

RI Australian tree frog Litoria xanthomera."

RL J. Pept. Sci. 3:181-185(1997).

CC -1- FUNCTION: HYPOTENSIVE NEUROPEPTIDE

CC -1- TISSUE SPECIFICITY: SECRETED BY THE SKIN DORSAL GLANDS.

CC -1- MASS SPECTROMETRY: MW=1354; METHOD=FAB.

CC -1- SIMILARITY: BELONGS TO THE GASTRIN/CHOLESTYKININ FAMILY.

InterPro: IPR001651; Gastrin.

PROSITE: PS00259; Gastrin; 1.

KW Amphibian skin: Hypotensive agent: Amidation. Sulfation.

FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.

FT MOD_RES 4 4 SULFATION.

FT MOD_RES 10 10 AMIDATION.

SQ SEQUENCE 10 AA: 1290 MW: 9905637861864A CRC64;

Query Match 40.0%; Score 2; DB 1; Length 10;

Best Local Similarity 100.0%; Pred. No. 4.4e+03;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 YT 5

DB 4 YT 5

RESULT 15

GONL_ALLMI STANDARD: PRT: 10 AA.
 AC P37041; P20407.
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE Gonadoliberin I (Gonadotropin-releasing hormone I) (GnRH-I) (LH-RH I)

DE (Lultherin I).
 CS Alligator mississippiensis (American alligator).
 CC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
 CC Archosauria; Crocodylia; Alligatorinae; Alligator.
 OX NCBI_TaxID=4466;

RN [1]

RP SEQUENCE.

PC TISSUE=Brain;

EX MEDLINE=9132336; PubMed=1882082;

EA Lowrey E.A., Fischer W.H., Fisher G.B., McEwen J.E., Park M.

RA Lance V., Swanson P., Rivier J.E., Sherwood N.M.;

RT "Primary structure of two forms of gonadotropin-releasing hormone

from brains of the American alligator (Alligator mississippiensis).";

REPL. Pept. 33:105-116(1991).

CC -1- FUNCTION: STIMULATES THE SECRETION OF GONADOTROPINS.

CC -1- SUBCELLULAR LOCATION: Secreted.

CC -1- SIMILARITY: BELONGS TO THE GnRH FAMILY.

DR PIR: A00066; RHAQ1.

DR InterPro: IPR002012; GnRH.

DR Pfam: PF00446; GnRH; 1.

DR PROSITE: PS00473; GnRH; 1.

KW Hormone: Amidation; Hypothalamus.

FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.

FT MOD_RES 10 10 AMIDATION.

SQ SEQUENCE 10 AA: 1172 MW: 28482307286845A3 CRC64;

Query Match 40.0%; Score 2; DB 1; Length 10;

Best Local Similarity 100.0%; Pred. No. 4.3e+03;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SY 4

DB 4 SY 5

Search completed: April 29, 2003, 08:52:28

Job time : 13.6667 secs


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DT 01-FEB-1997 (TRENBLrel. 02, Created)
DT 01-FEB-1997 (TRENBLrel. 02, Last sequence update)
DT 01-FEB-2001 (TRENBLrel. 12, Last annotation update)
DE Alginatase lyase (Fragment).
GN ALY.
OS Pseudomonas sp. (strain OS-ALG-9).
OC Bacteria; Proteobacteria.
OX NCBI_TaxID=86038;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=OS-ALG-9;
RA Fujiyama K.;
RL Submitted (01-1994) to the EMBL/GenBank/Tran databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=OS-ALG-9;
RA Maki H., Mori A., Fujiyama K., Kinoshita S., Yoshida T.;
FI "Cloning, sequence analysis and expression of Escherichia coli algA gene encoding an alginatase lyase from Pseudomonas sp. OS-ALG-9."
J. Gen. Microbiol. 139:987-993(1993)
EMBL: D38469; HAA21704.1; -
KW lyase.
FT NON-TER 1 1
FT NON-TER 8 8
SQ SEQUENCE 8 AA: 841 MW: 461DDDC5A5B041ER KC64;

Query Match 40.0%; Score 2; DB 4; Length 8;
Best Local Similarity 100.0%; Pred. No. 6.7e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 YT 5
DB 1 YT 2

RESULT 4
QYRX0
ID QYRX0 PRELIMINARY: PRT: 6 AA.
AC QYRX0;
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 01-MAY-2001 (TRENBLrel. 16, Last annotation update)
DE Ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (Fragment).
GN RBCL.
OS Bacteria; Cyanobacteria; Oscillatoriales; Planctothrix.
OX NCBI_TaxID=59312;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BC-PLA 9316, AND BC-PLA 9309;
RX MEDLINE=20005589; PubMed=10537197;
RA Beard S.J., Handley B.A., Hayes P.K., Walsh A.E.;
RT "The diversity of gas vesicle genes in Planctothrix rubescens from Lake Zurich."
RL Microbiology 145:2757-2768(1999).
DR EMBL: AJ13249; CAB59537.1; -
DR EMBL: AJ13248; CAB59534.1; -
FT NON-TER 1 1
FT NON-TER 8 AA: 957 MW: 3301AAAF8FE82CP KC64;
SQ SEQUENCE 8 AA: 957 MW: 3301AAAF8FE82CP KC64;

Query Match 40.0%; Score 2; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 6.7e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ES 3
DB 3 ES 4

RESULT 4
QYXJ4
DT 01-AUG-1998 (TRENBLrel. 07, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)

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ID QYXJ4 PRELIMINARY: PRT: 8 AA.
AC QYXJ4;
DT 01-NOV-1999 (TRENBLrel. 12, Created)
DT 01-NOV-1999 (TRENBLrel. 12, Last sequence update)
DT 01-NOV-1999 (TRENBLrel. 12, Last annotation update)
DE runt/WTG8 protein (Fragment).
GN RNT/WTG8.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Euthera; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95002916; PubMed=7919324;
RA Tigue J.E., Calabi F.;
RT "Alternative, out-of-frame runt/WTG8 transcripts are encoded by the derivative (6) chromosome in the t(8;21) of acute myeloid leukemia M2."
FI Blood 84:2115-2121(1994).
DR EMBL: S74092; AAD14144.1; -
FT NON-TER 1 1
FT NON-TER 8 AA: 1967 MW: 20F414044H17244R QPC64;
SQ SEQUENCE 8 AA: 1967 MW: 20F414044H17244R QPC64;

Query Match 40.0%; Score 2; DB 4; Length 8;
Best Local Similarity 100.0%; Pred. No. 6.7e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LE 2
DB 3 LE 4

RESULT 5
QYXJ3
ID QYXJ3 PRELIMINARY: PRT: 8 AA.
AC QYXJ3;
DT 01-NOV-1999 (TRENBLrel. 12, Created)
DT 01-NOV-1999 (TRENBLrel. 12, Last sequence update)
DT 01-NOV-1999 (TRENBLrel. 12, Last annotation update)
DE runt/WTG8 protein (Fragment).
GN RNT/WTG8.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Euthera; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=BONE MARROW;
RX MEDLINE=95002916; PubMed=7919324;
RA Tigue J.E., Calabi F.;
RT "Alternative, out-of-frame runt/WTG8 transcripts are encoded by the derivative (3) chromosome in the t(8;21) of acute myeloid leukemia M2."
FI Blood 84:2115-2121(1994).
DR EMBL: S74094; AAD14973.2; -
FT NON-TER 1 1
FT NON-TER 8 AA: 229 MW: 30E764105P17344B QRC64;
SQ SEQUENCE 8 AA: 229 MW: 30E764105P17344B QRC64;

Query Match 40.0%; Score 2; DB 4; Length 8;
Best Local Similarity 100.0%; Pred. No. 6.7e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LE 2
DB 3 LE 4

RESULT 6
Q60773
ID Q60773 PRELIMINARY: PRT: 8 AA.
AC Q60773;
DT 01-AUG-1998 (TRENBLrel. 07, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)

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DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
 DE F1126310.1 (Parvalbumin) (Fragment)
 GN PVALB.
 OS Homo sapiens (Human).
 OC Eukaryota, Metazoa, Chordata, Vertebrata, Euteleostomi,
 CC Mammalia, Eutheria, Primates, Catarrhini, Hominoidea, Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA HG S.;
 RL Submitted (DEC-1999) to the EMBL/GenBank/CCDS databases.
 DP EMBL: 282184, CAB05699.3,
 FT NON_TER 1 1
 SQ SEQUENCE 8 AA: 845 MW: 94841.0027318455 kDa; 424;
 Query Match 40.0%; Score 2; DB 4; Length 8;
 Best Local Similarity 100.0%; Pred. No. 6.7e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 ES 3
 Db 7 ES 8
 RESULT 7
 Q94623 PRELIMINARY: PRT: 8 AA.
 AC Q94623;
 DT 01-FEB-1997 (TrEMBLrel. 02, Created)
 DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
 DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
 DE MSUSP-2 protein (Fragment).
 GN USP.
 OS Manduca sexta (Tobacco hawkmoth) (Tobacco hornworm).
 CC Eukaryota, Metazoa, Arthropoda, Tracheata, Hexapoda, Insecta;
 CC Pterygota, Neoptera, Endopterygota, Lepidoptera, Glossata, Ditrysia;
 CC Spingioidea, Spingidae, Spinginae, Manduca.
 OX NCBI_TaxID=7130;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA TISSUE=EPIDERMIS;
 FX MEDLINE=97165493; PubMed=9013254;
 RA Tiodra M., Huang J.Y., Malone F., Asahina M., Piddiford L.M.;
 RT Identification and mRNA developmental profiles of two ultrastructural
 RT isoforms in the epidermis and wings of Manduca sexta.;
 RL Insect Mol. Biol. 6:41-53(1997).
 DR EMBL: 057421, AAA64386.1,
 FT NON_TER 8 8
 SQ SEQUENCE 8 AA: 802 MW: 116558.0415476916 kDa; 464;
 Query Match 40.0%; Score 2; DB 5; Length 8;
 Best Local Similarity 100.0%; Pred. No. 6.7e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ES 3
 Db 6 ES 7
 RESULT 8
 Q9XSY1 PRELIMINARY: PRT: 8 AA.
 AC Q9XSY1;
 DT 01-NOV-1999 (TrEMBLrel. 12, Created)
 DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
 DT 01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
 DE Retinoblastoma protein (Fragment).
 GN RBL.
 OS Canis familiaris (Dog).
 CC Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
 CC Mammalia, Eutheria, Carnivora, Fissipedia, Canidae, Canis.
 OX NCBI_TaxID=9615;
 RN [1]

RP SEQUENCE FROM N.A.
 FX MEDLINE=97849323; PubMed=8894053;
 RA Venta P.J., Brouillette J.A., Yuzbasiyan-Gurkan V., Brewer G.J.;
 RT "Gene-specific universal mammalian sequence-tagged sites: application
 RT to the canine genome.";
 RL Biochem. Genet. 34:321-341(1996).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Venta P.J., Cao Y., Alexander L., Yuzbasiyan-Gurkan V.;
 RT "Dinucleotide repeat polymorphism in the canine retinoblastoma (RBL)
 RT gene.";
 RL Submitted (JUN-1999) to the EMBL/GenBank/CCDS databases.
 DP EMBL: AF155737, AAD38807.1,
 FT NON_TER 1 1
 SQ SEQUENCE 8 AA: 545 MW: 14258.0186767212 kDa; 424;
 Query Match 40.0%; Score 2; DB 6; Length 8;
 Best Local Similarity 100.0%; Pred. No. 6.7e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 ES 3
 Db 6 ES 7
 RESULT 9
 Q9XNP8 PRELIMINARY: PRT: 8 AA.
 AC Q9XNP8;
 DT 01-NOV-1999 (TrEMBLrel. 12, Created)
 DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
 DT 01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
 DE ATP synthase 6 (Fragment).
 GN ATP6.
 OS Bosophilus microplus (Cattle tick).
 CC Mitochondrion.
 CC Eukaryota, Metazoa, Arthropoda, Chelicerata, Arachnida, Acari;
 CC Parasitiformes, Ixodida, Ixodidae, Boophilus.
 OX NCBI_TaxID=6941;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA STRAIN=N;
 FX MEDLINE=9227243; PubMed=10389895;
 RA Campbell N.J.H., Barker S.C.;
 RT "The novel mitochondrial gene arrangement of the cattle tick,
 RT Boophilus microplus (Ixodidae) and its taxonomic significance";
 RL Mol. Biol. Evol. 16:732-740(1999).
 DR EMBL: AF110616; AAD28386.1,
 KW Mitochondrion.
 FT NON_TER 1 1
 SQ SEQUENCE 8 AA: 105 MW: 6580.4444444444 kDa; 424;
 Query Match 40.0%; Score 2; DB 8; Length 8;
 Best Local Similarity 100.0%; Pred. No. 6.7e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 ES 3
 Db 7 ES 8
 RESULT 10
 Q34909 PRELIMINARY: PRT: 8 AA.
 AC Q34909;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-DEC-1999 (TrEMBLrel. 19, Last annotation update)
 DE Cytochrome b (Fragment).
 OS Locusta migratoria (Migratory locust).
 CC Mitochondrion.
 CC Eukaryota, Metazoa, Arthropoda, Tracheata, Hexapoda, Insecta;

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OC Eukaryota, Metazoa, Echinodermata, Eleutherozoa, Echinozoa,
OC Echinozoa, Echinozoa, Echinozoa, Echinozoa, Echinozoa,
OC Diadema,
OX NCBI_TaxID=105359;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=GLA121 AND GLA124;
RX MEDLINE=21323357; PubMed=11430656;
RA Lessios H.A., Kessing B.D., Pearse J.S.;
RT "Population structure and speciation in tropical seas: global
RI phylogeography of the sea urchin Diadema.";
RL Curr. Genet. 11:625-630(1987).
DR EMBL: X05286; CAA38905.1; -.
KW Mitochondrion.
FT NON_TER 1 1
FT NON_TER 4 8
SQ SEQUENCE 8 AA: 1076 MW: 7018173846CAF2E3 CRC64:

Query Match 40.0%; Score 2; DB 8; Length 8;
Best Local Similarity 100.0%; Pred. No. 6.7e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

3 SY 4
11
2 SY 4

RESULT 11
QWFR5
ID QWFR5 PRELIMINARY: PRT: 8 AA
AC QWFR5;
DT 01-MAR-2002 (TREMBlrel. 20, Created)
DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
DE Cytochrome oxidase subunit II (fragment).
GN COI.
OS Diadema paucispinum.
OC Eukaryota, Metazoa, Echinodermata, Eleutherozoa, Echinozoa,
OC Echinozoa, Echinozoa, Echinozoa, Echinozoa, Echinozoa,
OC Diadema,
OX NCBI_TaxID=145530.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=H11;
RX MEDLINE=21323357; PubMed=11430656;
RA Lessios H.A., Kessing B.D., Pearse J.S.;
RT "Population structure and speciation in tropical seas: global
RI phylogeography of the sea urchin Diadema.";
RL Curr. Genet. 11:625-630(1987).
DR EMBL: X05286; CAA38905.1; -.
KW Mitochondrion.
FT NON_TER 1 1
FT NON_TER 4 8
SQ SEQUENCE 8 AA: 954 MW: 6418173846CAF2E3 CRC64:

Query Match 40.0%; Score 2; DB 8; Length 8;
Best Local Similarity 100.0%; Pred. No. 6.7e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 LE 2
11
6 LE 7

RESULT 12
QWFR5
ID QWFR5 PRELIMINARY: PRT: 8 AA
AC QWFR5;
DT 01-MAR-2002 (TREMBlrel. 20, Created)
DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
DE Cytochrome oxidase subunit II (fragment).
GN COI.
OS Diadema mexicanum.
OC Eukaryota, Metazoa, Echinodermata, Eleutherozoa, Echinozoa,
OC Echinozoa, Echinozoa, Echinozoa, Echinozoa, Echinozoa,
OC Diadema,
OX NCBI_TaxID=105358;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=DA9414, DA9441, DIAN125, DIAN126, DIAN131, CN2, AND CN4;
RX MEDLINE=21323357; PubMed=11430656;
RA Lessios H.A., Kessing B.D., Pearse J.S.;
RT "Population structure and speciation in tropical seas: global
RI phylogeography of the sea urchin Diadema.";
RL Curr. Genet. 11:625-630(1987).
DR EMBL: X05286; CAA38905.1; -.
KW Mitochondrion.
FT NON_TER 1 1
FT NON_TER 4 8
SQ SEQUENCE 8 AA: 1076 MW: 7018173846CAF2E3 CRC64:

Query Match 40.0%; Score 2; DB 8; Length 8;
Best Local Similarity 100.0%; Pred. No. 6.7e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 LE 2
11
6 LE 7

RESULT 13
QWFR5
ID QWFR5 PRELIMINARY: PRT: 8 AA
AC QWFR5;
DT 01-MAR-2002 (TREMBlrel. 20, Created)
DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
DE Cytochrome oxidase subunit II (fragment).
GN COI.
OS Diadema antillarum.
OC Eukaryota, Metazoa, Echinodermata, Eleutherozoa, Echinozoa,
OC Echinozoa, Echinozoa, Echinozoa, Echinozoa, Echinozoa,
OC Diadema,
OX NCBI_TaxID=105358;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=DA9414, DA9441, DIAN125, DIAN126, DIAN131, CN2, AND CN4;
RX MEDLINE=21323357; PubMed=11430656;
RA Lessios H.A., Kessing B.D., Pearse J.S.;
RT "Population structure and speciation in tropical seas: global
RI phylogeography of the sea urchin Diadema.";
RL Curr. Genet. 11:625-630(1987).
DR EMBL: X05286; CAA38905.1; -.
KW Mitochondrion.
FT NON_TER 1 1
FT NON_TER 4 8
SQ SEQUENCE 8 AA: 1076 MW: 7018173846CAF2E3 CRC64:

Query Match 40.0%; Score 2; DB 8; Length 8;
Best Local Similarity 100.0%; Pred. No. 6.7e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 LE 2
11
6 LE 7

```

```

KW Mitochondrion
FT NON_TER 1
SQ SEQUENCE 8 AA: 1037 MW: 701B173B46DDC2F0 CRC64;

Query Match 40.0%; Score 2; DB 8; Length 8;
Best Local Similarity 100.0%; Pred. No. 6.7e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LE 2
DB 6 LE 7

RESULT 14
QWRG3
ID QWRG3 PRELIMINARY; PRT: 8 AA;
AC QWRG3;
DT 01-MAR-2002 (TRENDRel. 20, Created)
DT 01-MAR-2002 (TRENDRel. 20, Last sequence update)
DT 01-MAR-2002 (TRENDRel. 20, Last annotation update)
CY Cytochrome oxidase subunit II (Fragment);
COIL;
DS Diadema mexicanum;
OS Mitochondrion;
OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
EC Echinoidea; Echinoidea; Diadematacea; Diadematoidea; Diademataidae;
OC Diadema;
OX NCBI_TaxID=105359;
RN [1]
RP SEQUENCE FROM N.A.;
RC STRAIN=C15; D3; D5; D6; CC66; G123; DM1; DM; AND DM71;
RX MEDLINE=21561534; PubMed=11703875;
RA Lessios H.A., Kessing B.D., Pearse J.S.;
RT "Population structure and speciation in tropical seas: global
phylogeography of the sea urchin Diadema.";
RL Evolution 55:955-975(2001);
RN [2]
RP SEQUENCE FROM N.A.;
RC STRAIN=C15; D3; D5; D6; CC66; G123; DM1; DM; AND DM71;
RX MEDLINE=21561534; PubMed=11703875;
RA Lessios H.A., Garrido M.J., Kessing B.D.;
RT "Demographic history of Diadema antillarum, a keystone herbivore on
Caribbean reefs.";
RL Proc. R. Soc. Lond., B. Biol. Sci. 268:2347-2353(2001);
DR EMBL; AY012908; AAL33837.1;
DR EMBL; AY012911; AAL33838.1;
DR EMBL; AY012913; AAL33839.1;
DR EMBL; AY012914; AAL33840.1;
DR EMBL; AY012919; AAL33842.1;
DR EMBL; AY012940; AAL33847.1;
DR EMBL; AY012949; AAL33849.1;
DR EMBL; AY012950; AAL33850.1;
DR EMBL; AY012951; AAL33851.1;
KW Mitochondrion;
FT NON_TER 1
SQ SEQUENCE 8 AA: 1037 MW: 701B173B46DDC2F0 CRC64;

Query Match 40.0%; Score 2; DB 8; Length 8;
Best Local Similarity 100.0%; Pred. No. 6.7e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LE 2
DB 6 LE 7

RESULT 15
QWRG3
ID QWRG3 PRELIMINARY; PRT: 8 AA;
AC QWRG3;
DT 01-MAR-2002 (TRENDRel. 20, Created)
DT 01-MAR-2002 (TRENDRel. 20, Last sequence update)
DT 01-MAR-2002 (TRENDRel. 20, Last annotation update)

```

```

DE Cytochrome oxidase subunit II (Fragment);
GN COIL;
OS Diadema paucispinum;
OG Mitochondrion;
OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
EC Echinoidea; Echinoidea; Diadematacea; Diadematoidea; Diademataidae;
OC Diadema;
OX NCBI_TaxID=145530;
RN [1]
RP SEQUENCE FROM N.A.;
RC STRAIN=H12; H13; H15; H16; H19; H15; AND H119;
RX MEDLINE=21323357; PubMed=11430656;
RA Lessios H.A., Kessing B.D., Pearse J.S.;
RT "Population structure and speciation in tropical seas: global
phylogeography of the sea urchin Diadema.";
RL Evolution 55:955-975(2001);
DR EMBL; AY012960; AAL33853.1;
DR EMBL; AY012961; AAL33854.1;
DR EMBL; AY012962; AAL33855.1;
DR EMBL; AY012963; AAL33856.1;
DR EMBL; AY012964; AAL33857.1;
DR EMBL; AY012965; AAL33858.1;
DR EMBL; AY012966; AAL33859.1;
KW Mitochondrion;
FT NON_TER 1
SQ SEQUENCE 8 AA: 1037 MW: 701B173B46DDC2F0 CRC64;

Query Match 40.0%; Score 2; DB 8; Length 8;
Best Local Similarity 100.0%; Pred. No. 6.7e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LE 2
DB 6 LE 7

Search completed: April 29, 2003, 08:53:21
Job time : 21.5843 secs

```

Result No.	Query %		Length	DB	ID	Description
	Match	Score				
1	5	100.0	5	20	AAV49695	HIV-1 gp120 induce
2	4	80.0	9	22	AAV98253	Human peptide #152
3	4	80.0	10	22	ABR55971	Vascular dementia-1
4	4	80.0	10	22	ABG62194	Human Aβ1-49 trypt
5	4	80.0	10	22	AAU58456	Dpi tryptic digest
6	4	80.0	10	22	AAU26102	Depression-Associat
7	3	60.0	4	19	AAV20715	Human neurofilamen
8	3	60.0	4	19	AAV20656	Human neurofilamen
9	3	60.0	4	22	AAE09624	Peptide for analys
10	3	60.0	5	8	AAV71550	AIDS virus recepto

CC monitoring the effect of therapy administered to a subject having VD.
 CC Nucleic acids encoding a VPI or inhibiting the function of a VPI are
 CC useful for the treatment of VD and for gene therapy.

XX SQ Sequence 10 AA:

Query Match 80.0%; Score 4; DB 22; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1,3e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LESY 4
 IIII
 Db 3 LESY 6

RESULT 4

ABR52194

ID ABR52194 standard; Peptide: 10 AA.

AC ABR52194.

08-FEB-2002 (first entry)

Human API-148 tryptic digest peptide #2.

Human; neuroprotective; neurotropic; gene therapy; vaccine;

Alzheimer's disease; Alzheimer's Disease-Associated Feature; AF;

Alzheimer's Disease-Associated Protein Isoform; API; tryptic digest;

Expression Reference Protein Isoform; ERPI; proteolysis.

XX OS Homo sapiens.

XX PN W0200175454-A2.

XX PD 11-OCT-2001.

XX PF 03-APR-2001; 2001W0-0510008.

XX PP 03-APR-2000; 2000MS-104504P

XX PR 26-NOV-2000; 2000MS-253647P.

XX PA (OXFO-) OXFORD GLYCOSCIENCES UK LTD.

XX PA (PF12) PFIZER INC.

XX PI Durham KL, Friedman DL, Herath HM, Kimmel LH, Parekh RR;

PI Potter DM, Rohlff C, Silber BM, Stiger TK, Sunderland PI;

PI Townsend RR, White F, Williams SA;

XX WPI: 2001-600484/74.

PI Screening for Alzheimer's disease in a mammalian by making
 PI two-dimensional array of a feature whose relative abundance correlates
 PI with disease, and comparing with abundance of the feature in samples of
 PI healthy persons -

XX Example; Page 43; 162pp; English.

XX The invention relates to methods for the screening, diagnosis and
 CC prognosis of Alzheimer's disease. The methods involve the detection
 CC of Alzheimer's Disease-Associated Features (AFs) and Alzheimer's
 CC Disease-Associated Protein Isoforms (APIs) in cerebrospinal fluid,
 CC serum or plasma. The abundance of the AFs and APIs is then
 CC normalised to an Expression Reference Protein Isoform (ERPI) in
 CC order to determine whether a patient is suffering from, or has
 CC a predisposition to, Alzheimer's Disease. The relative abundance of
 CC the AFs and APIs correlates with the severity of Alzheimer's Disease.
 CC The present sequence is a peptide produced from an API by proteolysis.

XX SQ Sequence 10 AA:

Query Match 80.0%; Score 4; DB 22; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1,3e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LESY 4
 IIII
 Db 3 LESY 6

RESULT 5

AAU28456

ID AAU28456 standard; Peptide: 10 AA.

XX AC AAU28456.

XX DT 03-JAN-2002 (first entry)

XX DE DPI tryptic digest peptide #53.

XX Human; depression associated protein isoform; tryptic digest peptide-
 KW hsp, cerebrospinal fluid, CSF, hsp, hsp, bipolar affective disorder;
 KW neuropsychiatric disorder; bipolar mood disorder; neuroleptic;
 KW manic-depressive illness; schizoaffective disorder.

XX OS Homo sapiens.

XX PR W0200162787-A1.

XX PD 30-AUG-2001.

XX PF 23-FEB-2001; 2001W0-060796.

XX PR 24-FEB-2000; 2000GB-0004112.

XX PR 04-DEC-2000; 2000GR-0030050.

XX PR 12-DEC-2000; 2000US-0254830.

XX PA (OXFO-) OXFORD GLYCOSCIENCES UK LTD.

XX PI Herath HM, Parekh RR, Rohlff C, Terrett JA, Tyson KL;

XX WPI: 2001-570626/64.

XX Novel nucleic acid encoding a protein associated with bipolar affective
 PT disorder, which is used for diagnosis, prophylaxis and therapy of
 PT neuropsychiatric disorders, such as bipolar affective disorder -

XX Disclosure; Page 31; 153pp; English.

XX The present invention relates to the identification of depression
 CC associated protein isoforms (DPIs), particularly the tryptic digest
 CC peptides of these proteins. Some of the DPIs (AAU28404-AAU28425)
 CC described are decreased in the cerebrospinal fluid (CSF) of hsp
 CC (bipolar affective disorder) subjects, whilst other DPIs
 CC (AAU28426-AAU28487) are increased in hsp subjects. Also described
 CC are peptide sequences identified from DPI-45 and DPI-213 and the
 CC nucleic acid sequences they are encoded by. The sequences of the
 CC invention are useful for clinical screening, diagnosis, prognosis,
 CC therapy and prophylaxis of neuropsychiatric disorders e.g. BAP (also
 CC known as bipolar mood disorder, BP), manic-depressive illnesses,
 CC attention deficit disorders, schizoaffective disorders, and unipolar
 CC affective disorders. The present sequence represents one of the DPI
 CC tryptic digest peptides of the present invention.

XX SQ Sequence 10 AA:

Query Match 80.0%; Score 4; DB 22; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1,3e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LESY 4
 IIII
 Db 3 LESY 6

RESULT 6

AAU26102

ID AAU26102 standard; Peptide: 10 AA
 XX AAU26102;
 AC
 XX
 DI 18-DEC-2001 (first entry)
 DE Depression-Associated Protein isoform DPI-1.
 DE
 XX Human, Bipolar Affective Disorder, BAD; Depression-Associated Protein
 XX DPI-1; Depression-Associated Protein isoform DPI-1; Cerebrospinal fluid;
 XX CSF; antidepressant; antimanic; neuroleptic; neuroleptic;
 XX attention deficient disorder; schizophrenia disorder;
 XX bipolar affective disorder;
 XX
 OS Homo sapiens.
 XX
 XX W0200163294-A2.
 XX
 XX 30-AUG-2001.
 XX
 XX 23-FEB-2001; 2001WO-0800791.
 XX
 XX 24-FEB-2000; 2000GH-0004412.
 XX 08-DEC-2000; 2000GB-0030050.
 XX 12-SEP-2000; 2000US-0254830.
 XX
 XX (OXFORD) EXP-PROGLY-SCIENCES UK LTD
 XX
 XX Herath HMAC, Parekh RB, Rohlf C;
 PI
 XX WPI: 2001-582081/65.
 XX
 XX Preparation for diagnosing or treating bipolar affected disorder (BAD)
 XX or unipolar depression, or for screening for modulators, comprises a
 XX BAD-associated protein isoform.
 XX
 XX Claim 8: Page 31; 163pp; English.
 XX
 XX The invention relates to a preparation comprising an isolated bipolar
 XX Affected Disorder (BAD)-Associated Protein isoform (DPI). The DPI's are
 XX used to screen, diagnose or prognosis of BAD or unipolar depression,
 XX determine the stage or severity of BAD or unipolar depression, identify a
 XX subject at risk of developing BAD or unipolar depression, or monitor the
 XX effect of therapy in a subject. They are also used to screen for or
 XX identify agents that interact with a DPI. These agents, antibodies
 XX against the DPIs, and nucleic acids encoding the DPIs are used to treat
 XX or prevent BAD or unipolar depression. Diseases that can be treated are
 XX attention deficient disorder, a schizophrenia disorder, a bipolar or a
 XX unipolar affective disorder. The DPIs are used in proteomics. The
 XX proteomic approach of using DPIs for screening, diagnosis or prognosis of
 XX BAD or unipolar depression overcomes the problems of using gene
 XX expression analysis, such as not being able to obtain central nervous
 XX system (CNS) tissue from a living patient under normal circumstances.
 XX The present sequence is a DIP decreased in the CSF (cerebrospinal
 XX fluid) of subjects having BAD.
 XX
 XX Sequence 10 AA:
 XX
 XX Query Match: 60.0%; Score 4; DB 10; Length 10;
 XX Best Local Similarity 100.0%; Pred No. 134012;
 XX Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 XX 1 LESY 4
 XX ||||
 XX 3 LESY 6
 XX
 XX RESULT 7
 XX AAY20715
 XX ID AAY20715 standard; Protein: 4 AA.
 XX AC
 XX AAY20715;
 XX

PI 22-NOV-1998 (first entry)
 XX
 DE Human neurofilament-M wild type protein fragment 57.
 XX
 XX Human; beta-amyloid precursor protein; beta-APP; diagnosis; cancer;
 KW frameshift mutation; age-related disease; neurodegenerative disorder;
 KW Alzheimer's disease; Down's syndrome; myotonic dystrophy; neuronal;
 KW Huntington's disease; multiple sclerosis; alcoholic liver disease;
 KW diabetes mellitus type II; microtubule associated protein; Tau; Big Tau;
 KW neurofilament; neurofilament E; MAP2; neurofilament; neurofilament-M;
 KW neurofilament-F; presenilin 1; presenilin 2; cellular; tumor; antigen;
 KW glial fibrillary acidic protein; GFAP; p53; semaphorin III; HSP-70;
 KW 1-12 k-cell tumour antigen; 2-12 k-cell antigen; HM60; HSP-70;
 KW high mobility group protein-C; neuroendocrine specific protein A.
 XX
 OS Homo sapiens.
 XX
 XX W09845322-A2.
 XX
 XX 15-OCT-1998.
 XX
 XX 02-APR-1998; 98WO-1B00705.
 XX
 XX 10-APR-1997; 97US-0043163.
 XX
 XX (UYUT-) RICKSUNIV UTRECHT.
 XX (UYUT-) ROYAL NETHERLANDS ACAD ARTS & SCI.
 XX (UYUT-) UNIV ROTTERDAM EPASMUS.
 XX
 XX Burbach JPH, Grosveld FG, Van Leeuwen FW;
 PI
 XX WPI: 1998-609901/51.
 XX N-PSDB: AAX75759.
 XX
 XX Diagnosing disease by detecting frameshift mutations in RNA or
 XX corresponding protein mutations - used to diagnose cancer and
 XX neurological diseases, particularly Alzheimer's disease, and also
 XX for treatment and prevention with specific ribozymes or wild-type
 XX RNA
 XX
 XX Disclosure: Figure 8; 258pp; English.
 XX
 XX This invention describes a novel method for the diagnosis of a disease
 XX caused by, or associated with, an RNA molecule that has a frameshift
 XX mutation. The method is used to diagnose age-related diseases, especially
 XX cancer and a wide range of neurodegenerative disorders (e.g. Alzheimer's
 XX disease, Down's syndrome, myotonic dystrophy, Huntington's disease,
 XX multiple sclerosis, alcoholic liver disease, diabetes mellitus type II
 XX and many others listed), or susceptibility to these disorders. The method
 XX allows a definitive diagnosis of Alzheimer's disease in living patients.
 XX at an early stage. It is based on the observation that disease may be
 XX caused by mutations in RNA rather than DNA. The invention describes the
 XX used of neuronal system RNA molecules, specifically proteins including
 XX beta amyloid precursor protein (beta-APP), the microtubule associated
 XX proteins Tau and Big Tau, ubiquitin B, apolipoprotein E, microtubule
 XX associated protein 2 (MAP2), neurofilament-L, neurofilament-M,
 XX neurofilament-F, presenilin 1, presenilin 2, glial fibrillary acidic
 XX protein (GFAP), the cellular tumour antigen p53, B-cell leukemia/lymphoma
 XX 2 (BCL2), 12-O-tetradecanoyl phorbol-13-acetate 12-O-tetradecanoyl group
 XX protein-C (HMGP-C) and neuroendocrine specific protein A.
 XX
 XX Sequence 4 AA:
 XX
 XX Query Match: 60.0%; Score 3; DB 19; Length 4;
 XX Best Local Similarity 100.0%; Pred No. 780-05;
 XX Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 XX 2 ESY 4
 XX ||||
 XX 1 ESY 3
 XX
 XX RESULT 8

AAY20655
 ID AAY20655 standard; Protein; 4 AA.
 AC AAY20655;
 XX
 XX
 DT 22-JUL-1999 (first entry)
 DE Human neurofilament-L wild type protein fragment 46.
 DE
 DE
 XX
 KW Human; beta-amyloid precursor protein; beta-A4; diagnosis: cancer;
 KW frameshift mutation; age-related disease; neurodegenerative disorder;
 KW Alzheimer's disease; Down's syndrome; myotonic dystrophy; neuronal;
 KW Huntington's disease; multiple sclerosis; alcohol liver disease;
 KW diabetes mellitus type II; microtubule associated protein; Tau; Big Tau;
 KW ubiquitin B; apolipoprotein E; MAP2; neurofilament-L; neurofilament-M;
 KW neurofilament-F; presenilin 1; presenilin 11; cellular tumour antigen;
 KW glial fibrillary acidic protein; GFAP; p53; smaphorin III; HSPF-1;
 KW bel-2; B-cell leukemia/lymphoma 2 proto-oncogene; HMGP-C; NSP-A;
 KW high mobility group protein-C; neuroendocrine specific protein A.
 XX
 XX Homo sapiens.
 C;
 PR W09845322-A2.
 XX
 XX
 PU 15-OCT-1998.
 XX
 DE 02-APR-1998: 98WO-1B00705
 XX
 XX 10-APR-1997: 670S-0043163.
 PR
 XX (UYUT-) PIJRSUNIV UTRECHT.
 PA (ROYA-) ROYAL NETHERLANDS ACAD APTS & SCI.
 PA (UYRO-) UNIV ROTTERDAM ERASMUS.
 XX
 FI Rurbach JPH, Grosveld FG, Van Leeuwen FW;
 XX
 XX WPI: 1998-60990/51.
 DE N-PSDB: AAX75758.
 DR
 XX
 PT Diagnosing disease by detecting frameshift mutations in RNA or
 PT corresponding protein mutations - used to diagnose cancer and
 PT neurological diseases, particularly Alzheimer's disease, and also
 PT for treatment and prevention with specific polymers of wild-type
 PT RNA
 PS Disclosure: Figure 7: 258pp; English.
 XX
 CC This invention describes a novel method for the diagnosis of a disease-
 CC caused by, or associated with, an RNA molecule that has a frameshift
 CC mutation. The method is used to diagnose age related diseases, especially
 CC cancer and a wide range of neurodegenerative disorders (e.g. Alzheimer's
 CC disease, Down's syndrome, myotonic dystrophy, Huntington's disease,
 CC multiple sclerosis, alcoholic liver disease, diabetes mellitus type II
 CC and many others listed) or susceptibility to these disorders. The method
 CC allows a definitive diagnosis of Alzheimer's disease in living patients,
 CC at an early stage. It is based on the observation that disease may be
 CC caused by mutations in RNA rather than DNA. The invention describes the
 CC use of neuronal system RNA molecules, specifically proteins including
 CC beta-amyloid precursor protein (beta-A4), the microtubule associated
 CC proteins Tau and Big Tau, ubiquitin B, apolipoprotein E, microtubule
 CC associated protein 2 (MAP2), neurofilament-L, neurofilament-M,
 CC neurofilament-F, presenilin 1, presenilin 11, glial fibrillary acidic
 CC protein (GFAP), the cellular tumour antigen p53, B-cell leukemia/lymphoma
 CC 2 (bel-2) proto-oncogene, smaphorin III, HSPF-1, high mobility group
 CC protein-C (HMGP-C) and neuroendocrine specific protein A.
 XX
 XX Sequence 4 AA:
 S0
 Query Match 60.0%; Score 3; DB 19; Length 4;
 Best Local Similarity 100.0%; Pred. No. 7,8e-05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 SYT 5

DB 1 SYT 3
 III
 RESULT 9
 AAE08624
 ID AAE08624 standard; peptide; 4 AA.
 XX
 AC AAE08624;
 XX
 XX
 DT 01-NOV-2001 (first entry)
 DE Peptide for analysis; T-cell proliferative activity of human p35/p40.
 DE
 DE
 XX Cytokines T-cell; interferon-gamma; IFN gamma; bacterial infection;
 KW AIDS; diabetic retinopathy; cancer vaccine; cell-mediated immunity;
 KW p35; p40.
 KW
 KW Synthetic.
 CS
 XX W0200140257-A2.
 PN
 XX
 XX 07-JUN-2001.
 PD
 XX 30-NOV-2000; 2000WO-US32664.
 PF
 XX 02-DEC-1999; 99US-0159035.
 PP
 PR 28-NOV-2000; 2000US-0159035.
 XX
 XX (MAXY-) MAXYGEN INC.
 PA
 XX Leong SK, Punnonen J;
 PI
 XX WPI: 2001-502381/55.
 DR
 XX
 XX Nucleic acids encoding modified cytokine polypeptides (i.e. modified
 PT p40 and p35 polypeptides), useful for treating various diseases e.g.
 PT diabetic retinopathy and cancer.
 PT
 XX Disclosure: Page 41: 223pp; English.
 ES
 XX The invention relates to nucleic acids encoding modified cytokine
 CC polypeptides (i.e. modified p40 and p35 polypeptides), the modified
 CC cytokine polypeptides have T-cell proliferative and interferon (IFN)-
 CC gamma induction activities. The polypeptides and polynucleotides of the
 CC invention are useful for treating various diseases e.g. bacterial
 CC infections, AIDS, diabetic retinopathy and cancer. The polypeptide and
 CC polynucleotide may also be useful as a vaccine adjuvant, to enhance a
 CC vaccinated host's cell-mediated immunity for protective response to a
 CC pathogen. The present sequence is a peptide used in the study of
 CC T-cell proliferative activity of human cytokine p35/p40.
 XX
 S0 Sequence 4 AA:
 Query Match 60.0%; Score 3; DB 22; Length 4;
 Best Local Similarity 100.0%; Pred. No. 7,8e-05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LES 3
 III
 DB 1 LES 3
 RESULT 10
 AAF71550
 ID AAF71550 standard; Protein; 5 AA.
 XX
 AC AAF71550;
 AC
 XX
 DT 07-MAY-1991 (first entry)
 DE
 DE AIDS virus receptor site blocking peptide (III).
 DE
 XX

KW AIDS: virus, receptor site, HIV, vaccine, antibodies.

XX Synthetic.

XX EP249390-A.

XX 16-DEC-1987.

XX 03-JUN-1987; 87EP-0304913.

XX 11-MAY-1987; 87US-0048148.

XX 04-JUN-1986; 86US-0869919.

XX 26-JUN-1986; 86US-0878586.

XX 12-DEC-1986; 86US-0940919.

XX 03-JUN-1987; 87EP-0304913.

XX (PERT/) PERT C B.

XX (USDC) US SEC OF COMMERCE.

XX Pert CB, Ruff MR, Farrar WL;

XX WPI: 1987-350068/50.

XX New peptide(s) related to AIDS virus - which inhibit AIDS virus

XX binding to receptor sites and prevent cell infectivity with AIDS

XX virus

XX Claim 5; Page 9; 12pp; English.

XX This peptide is a specifically claimed example of a highly

XX generic formula.

XX The peptide blocks effectively receptor sites of

XX cells and prevents cell infectivity with AIDS virus in monkey, rat

XX and human brain membranes and cells of the immune system.

XX Vaccine preps. contg. the peptide provide protection against

XX infection by AIDS virus. The peptide can also be used in kits for

XX the detection of the AIDS virus and antibodies to the AIDS virus;

XX and as immunogens to elicit monoclonal antibodies.

XX The peptide may be produced by conventional methods of peptide

XX synthesis using solid phase or liquid phase methods.

XX See also AAP71548-56, and EP-249394.

XX Sequence 5 AA;

XX Query Match 60.0%; Score 3; DB 8; Length 5;

XX Best Local Similarity 100.0%; Pred. No. 7 8e+05;

XX Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX 3 SYT 5

XX III

XX 3 SYT 5

XX Db

XX RESULT 11

XX AAP71551

XX ID AAP71551 standard; Protein: 5 AA.

XX AC AAP71551;

XX XX 07-MAY-1991 (first entry)

XX XX AIDS virus receptor site blocking peptide (IV).

XX XX AIDS: virus; receptor site; HIV; vaccine; antibodies.

XX XX Synthetic.

XX XX EP249390-A.

XX XX 16-DEC-1987.

XX XX 03-JUN-1987; 87EP-0304913

XX XX

PR 11-MAY-1987; 87US-0048148.

PR 03-JUN-1986; 86US-0869919.

PR 26-JUN-1986; 86US-0878586.

PR 12-DEC-1986; 86US-0940919.

PR 03-JUN-1987; 87EP-0304913.

XX (PERT/) PERT C B.

XX (USDC) US SEC OF COMMERCE.

XX Pert CB, Ruff MR, Farrar WL;

XX WPI: 1987-350068/50.

XX New peptide(s) related to AIDS virus - which inhibit AIDS virus

XX binding to receptor sites and prevent cell infectivity with AIDS

XX virus

XX Claim 5; Page 9; 12pp; English.

XX This peptide is a specifically claimed example of a highly

XX generic formula.

XX The peptide blocks effectively receptor sites of

XX cells and prevents cell infectivity with AIDS virus in monkey, rat

XX and human brain membranes and cells of the immune system.

XX Vaccine preps. contg. the peptide provide protection against

XX infection by AIDS virus. The peptide can also be used in kits for

XX the detection of the AIDS virus and antibodies to the AIDS virus;

XX and as immunogens to elicit monoclonal antibodies.

XX The peptide may be produced by conventional methods of peptide

XX synthesis using solid phase or liquid phase methods.

XX See also AAP71548-56, and EP-249394.

XX Sequence 5 AA;

XX Query Match 60.0%; Score 3; DB 8; Length 5;

XX Best Local Similarity 100.0%; Pred. No. 7 8e+05;

XX Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX 3 SYT 5

XX III

XX 3 SYT 5

XX Db

XX RESULT 12

XX AAP83009

XX ID AAP83009 standard; protein, 5 AA.

XX AC AAP83009;

XX XX 10-DEC-1990 (first entry)

XX XX Blocking peptide used in composition for treatment and diagnosis

XX DE of HIV infections.

XX XX HIV; gp120; monoclonal antibodies; neutralising region.

XX XX Homo sapiens.

XX XX GB2196634-A.

XX XX 05-MAY-1988.

XX XX 19-AUG-1987; 87GB-0719587.

XX XX 29-JUN-1987; 87US-0067996.

XX XX 01-MAY-1987; 87US-0045026.

XX XX 20-AUG-1986; 86US-0898273.

XX XX (GENE-) GENETIC SYSTEMS COR.

XX XX WPI: 1988-103268/15.

XX XX Monoclonal antibodies and peptide(s) useful for treatment and

XX XX

PT diagnosis of human immunodeficiency virus infections
 XX Claim 42; Page 24; 25pp; English.
 XX
 XX This is a blocking peptide which inhibits virus proliferation.
 CC It is useful, in conjunction with a monoclonal antibody to a
 CC neutralising region of HIV, for treatment or prophylaxis of HIV
 CC infections. N- and C-terminals can have up to 20 amino acids attached.
 CC See also AAP84003-08 and AAP84010-12.
 CC This is equivalent to NL8761959 (accession no. is from this).
 XX
 XX Sequence 5 AA:
 SQ

Query Match 60.0%; Score 3; DP 9; Length 5;
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SYT 5
 III
 Db 3 SYT 5

RESULT 13
 AAP91855
 ID AAP91855 standard; protein: 5 AA.
 XX
 XX AAP91855;
 AC
 XX 17-DEC-2001 (updated)
 DT 22-MAY-1990 (first entry)
 DT
 XX Pentapeptide which inhibits HIV binding to cell surface receptors.
 DE
 XX HIV; psoriasis; neuropsychiatric disorders.
 KW
 XX
 XX USN7352313-N.
 PN
 XX 10-OCT-1989.
 PD
 XX 16-MAY-1989; E90S-0212648.
 PF
 XX 16-MAY-1989; E90S-0352313.
 PR
 XX (USSH) US DEPT HEALTH AND HUMAN.
 PA
 XX Bridge P, Goodwin FR.
 PI
 XX WPI: 1989-378087-51.
 PR

Use of short peptide(s) to inhibit binding of HIV to human cells for
 treating psoriasis and neuropsychiatric disorder including memory
 deficiency and mood disorder.

PS Disclosure; Page 8; 18pp; English.
 XX

This peptide is used in a composition for treatment of brain conditions
 eg neuropsychiatric disorders and psoriasis through inhibition of HIV
 cell surface receptor (CD4) binding. CD4 site is common to the CNS and
 immune system. AIDS- and non AIDS-related psoriasis both respond
 favourably to treatment with the peptide-containing composition. There
 are a range of forms which the composition and administration can take.
 The serine residue can be replaced by an asparagine residue. Analogues
 of these peptides with D-threonine as the amino-terminal residue and/or
 an amide derivative at the carboxy-terminal can also be used.
 CC (Note: Revised entry submitted to correct the patent number format of
 CC US Government-owned NTIS applications to prevent clashes with ongoing US
 CC granted patent numbers. For further information please visit the Derwent
 CC web site at www.derwent.com/dwpl/updates/ntis-us.html)
 XX
 XX Sequence 5 AA:
 SQ

Query Match 60.0%; Score 3; DP 10; Length 5;
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SYT 5
 III
 Db 3 SYT 5

RESULT 15
 AAR28941
 ID AAR28941 standard; peptide: 5 AA.

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SYT 5
 III
 Db 3 SYT 5

RESULT 14
 AAR26903
 ID AAR26903 standard; peptide: 5 AA.
 XX
 XX AAR26903;
 AC
 XX 20-MAY-1998 (first entry)
 DT
 XX Herpes simplex virus treatment peptide.
 DE
 XX
 XX HSV; HSV-1; HSV-2; Varicella Zoster virus; human cytomegalovirus;
 KW Epstein-Barr virus.
 KW
 XX Synthetic.
 OS
 XX WC9214751-A.
 PN
 XX 03-SEP-1992.
 PD
 XX 24-FEB-1992; 92WO-DE00053.
 PF
 XX 25-FEB-1991; 91DK-0000319.
 PR
 XX (CARL-) CARLBIOTECH LTD-AS.
 PA
 XX Macfadden DK, Pedersen G.
 PI
 XX WPI: 1992-315120/38.
 DR
 XX
 XX New linear or cyclic peptide(s) including cysteine residue
 PT occupy lymphocyte CD4 receptors, for treating and preventing
 PT virus infections with Herpes simplex, Varicella Zoster,
 PT cytomegalovirus and Epstein-Barr virus
 XX
 XX Claim 5; Page 15; 21pp; English.
 XX

The peptide is useful in the treatment and prevention of diseases or
 conditions caused by Herpes viruses, esp. Herpes Simplex Virus-1
 (HSV-1), HSV-2, Varicella Zoster Virus (VZV), human cytomegalovirus
 (HCMV) or Epstein-Barr Virus (EBV). It can also be used to treat
 diseases and conditions caused by the family of herpes viruses in
 animals, e.g. AIDS-like disease in pigs, bovine rhinotracheitis
 and lymphangitis in horses. Lymphotracheitis in poultry and Marek's
 disease in chickens. It can also be used in diagnostics. The peptide
 has never been reported to penetrate any type of cells, but only to
 occupy the CD4 receptors found on lymphocytes and it apparently
 penetrates the skin with relative ease. A major advantage of the
 CC peptide is its almost complete lack of toxicity, which means that the
 CC use of high doses for an extended period of time is possible without
 CC any drawbacks. It is an example of a highly generic peptide
 CC (AAR26903-5). See also AAR26901-AAR26906.
 XX
 XX Sequence 5 AA:
 SQ

Query Match 60.0%; Score 3; DP 13; Length 5;
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SYT 5
 III
 Db 3 SYT 5

RESULT 15
 AAR28941
 ID AAR28941 standard; peptide: 5 AA.

XX AAR28941;
XX 23-MAR-1993 (first entry)
XX Example of a generic peptide for treating chronic fatigue syndrome.
DE CFS; fatigue; tension; anger; confusion; peptide T; HIV; synthetic;
KW human immunodeficiency virus; gp 120.
XX Synthetic.
XX Key Location/Qualifiers
FH Misc-difference 1 /note- "Thr or D-Thr"
FT Modified-site 5 /note- "may be amidated"
FI
FI
XX WO9219257-A.
FN
12-NOV-1992.
XX 08-MAY-1992; 92WO-US03582.
XX 08-MAY-1991; 91US-0696556.
XX (USSH) US DEPT HEALTH & HUMAN SERVICE.
XX Bridge TP. Goodwin PK;
XX WPI: 1992-398545/48.
XX Peptide compsns. for treating chronic fatigue syndrome.
PT ameliorate symptoms and improve vigour and cognitive and
PT neuro-motor performance
XX Disclosure; Page 4; Zipp; English.
XX The synthetic peptide is an example of a generic peptide whose
sequence is based on the sequence of peptide T, a sub region of
CC HIV gp120 responsible for binding to brain membrane and human T
CC cells. The peptide may be used for treatment of chronic fatigue
CC syndrome not associated with HIV infection. The peptide will reduce
CC fatigue, tension, anger and confusion and improves cognitive and
CC neuromotor performance.
CC See also AAR28918-42.
XX

Sequence 5 AA;
Query Match 60.0%; Score 3; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 7.8e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3 SYT 5
DB 3 SYT 5

Search completed: April 29, 2003, 08:51:53
Job time : 44.0833 secs


```

Db      3 LESY 6

RESULT 2
US-09-848-967-6
: Sequence 46, Application US/09791393
: Publication No. US20030032200A1
: GENERAL INFORMATION:
: APPLICANT: Herath, Herath Mudiyanselage Athula Chandrasiri
: APPLICANT: Parakkh, Rajesh Bhikhu
: APPLICANT: Rohlf, Christian
: TITLE OF INVENTION: Proteins, Genes and Their Use for
: TITLE OF INVENTION: Diagnosis and Treatment of Bipolar Affective Disorder (BAP)
: FILE REFERENCE: 2543-1-001 N1
: CURRENT FILING DATE: 2003-01-02
: CURRENT APPLICATION NUMBER: US/09791393
: EARLIER FILING DATE: 2003-01-02
: EARLIER APPLICATION NUMBER: GB 0004412.3
: EARLIER FILING DATE: 2003-02-24
: EARLIER APPLICATION NUMBER: GB 0030050.9
: EARLIER FILING DATE: 2000-12-08
: EARLIER APPLICATION NUMBER: US 60/254,830
: EARLIER FILING DATE: 2000-12-12
: NUMBER OF SEQ ID NOS: 308
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 46
: LENGTH: 10
: TYPE: PRT
: ORGANISM: Homo sapiens
US-09-848-967-6

Query Match      80.0%  Score 4; DB 9; Length 10;
Best Local Similarity 100.0%  Pred. No. 43;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 LESY 4
       1111
Db      3 LESY 6

RESULT 3
US-09-791-389-46
: Sequence 46, Application US/09791393
: Publication No. US20030032773A1
: GENERAL INFORMATION:
: APPLICANT: Herath, Herath Mudiyanselage Athula Chandrasiri
: APPLICANT: Parakkh, Rajesh Bhikhu
: APPLICANT: Rohlf, Christian
: APPLICANT: Tetter, Jonathan Alexander
: APPLICANT: Tyson, Kerry Louise
: TITLE OF INVENTION: Proteins, Genes and Their Use for
: TITLE OF INVENTION: Diagnosis and Treatment of Bipolar Affective Disorder (BAP)
: FILE REFERENCE: 2543-1-001 N2
: CURRENT FILING DATE: 2003-02-23
: PRIOR APPLICATION NUMBER: GB 0004412.3
: PRIOR FILING DATE: 2003-02-24
: PRIOR APPLICATION NUMBER: GB 0030050.9
: PRIOR FILING DATE: 2000-12-08
: PRIOR APPLICATION NUMBER: US 60/254,830
: PRIOR FILING DATE: 2000-12-12
: NUMBER OF SEQ ID NOS: 308
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 46
: LENGTH: 10
: TYPE: PRT
: ORGANISM: Homo sapiens
US-09-791-389-46

Query Match      80.0%  Score 4; DB 9; Length 10;
Best Local Similarity 100.0%  Pred. No. 43;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 LESY 4
       1111
Db      3 LESY 6

RESULT 4
US-09-791-393-46
: Sequence 46, Application US/09791393
: Publication No. US20030032200A1
: GENERAL INFORMATION:
: APPLICANT: Herath, Herath Mudiyanselage Athula Chandrasiri
: APPLICANT: Parakkh, Rajesh Bhikhu
: APPLICANT: Rohlf, Christian
: TITLE OF INVENTION: Proteins, Genes and Their Use for
: TITLE OF INVENTION: Diagnosis and Treatment of Bipolar Affective Disorder (BAP)
: FILE REFERENCE: 2543-1-001 N1
: CURRENT FILING DATE: 2003-01-02
: CURRENT APPLICATION NUMBER: US/09791393
: EARLIER FILING DATE: 2003-01-02
: EARLIER APPLICATION NUMBER: GB 0004412.3
: EARLIER FILING DATE: 2003-02-24
: EARLIER APPLICATION NUMBER: GB 0030050.9
: EARLIER FILING DATE: 2000-12-08
: EARLIER APPLICATION NUMBER: US 60/254,830
: EARLIER FILING DATE: 2000-12-12
: NUMBER OF SEQ ID NOS: 308
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 46
: LENGTH: 10
: TYPE: PRT
: ORGANISM: Homo sapiens
US-09-791-393-46

Query Match      80.0%  Score 4; DB 9; Length 10;
Best Local Similarity 100.0%  Pred. No. 43;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 LESY 4
       1111
Db      3 LESY 6

RESULT 5
US-09-071-838-247
: Sequence 47, Application US/09071838
: Patent No. US20020152501A1
: GENERAL INFORMATION:
: APPLICANT: Fischer, Robert L.
: APPLICANT: Ohad, Nir
: APPLICANT: Kiyosue, Tomohiro
: APPLICANT: Yadehara, Ramin
: APPLICANT: Margossian, Linda
: APPLICANT: Harada, John
: APPLICANT: Goldberg, Robert B.
: TITLE OF INVENTION: Nucleic Acids That Control Seed and
: TITLE OF INVENTION: Fruit Development in Plants
: NUMBER OF SEQUENCES: 324
: CORRESPONDENCE ADDRESS:
: ADDRESS: Townsend and Townsend and Crew LLP
: STREET: Two Embarcadero Center, Eighth Floor
: CITY: San Francisco
: STATE: California
: COUNTRY: USA
: ZIP: 94111-3834
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: ALTERNATIVE NUMBER: US 02/071,838
: FILING DATE: 01-MAY-1998
: CLASSIFICATION: R00
: AITOFNEY/AGENT INFORMATION:
: NAME: Bastian, Kevin L.
: REGISTRATION NUMBER: 34,774
: REFERENCE/DOCET NUMBER: 023070-0961000S
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (415) 576-0200

```

TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 247:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-071-838-247

Query Match 60.0%, Score 3, DB 10, Length 4:
Best Local Similarity 100.0%, Pred. No. 2,7e-05, Indels 0,
Matches 3, Conservative 3, Mismatches 0, Gaps 0,

QY 3 SYT 5
DB 1 SYT 3

US-09-286-240-20
Sequence 20, Application US/99286240
Patent No. US2002010420A1
GENERAL INFORMATION:
APPLICANT: Pett, James W

TITLE OF INVENTION: Chimeric and Humanized Antibodies to Angiostatin
FILE REFERENCE: 10498/740/3
CURRENT APPLICATION NUMBER: US/99/286,240
CURRENT FILING DATE: 1999-04-05

NUMBER OF SEQ ID NOS: 25
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 20
LENGTH: 5
TYPE: PRT
ORGANISM: Mus musculus
FEATURE:

US-09-286-240-20

Query Match 60.0%, Score 3, DB 10, Length 5:
Best Local Similarity 100.0%, Pred. No. 2,7e-05, Indels 0,
Matches 3, Conservative 0, Mismatches 3, Gaps 0,

QY 3 SYT 5
DB 1 SYT 3

US-09-828-708-17
Sequence 17, Application US/99828708
Patent No. US20020146753A1
GENERAL INFORMATION:
APPLICANT: Dittel, H.

APPLICANT: Bottom, D.
APPLICANT: Schaller, M.
TITLE OF INVENTION: Autoantibodies to glucose 6-phosphate isomerase and their partici
FILE REFERENCE: 1361.005051
CURRENT APPLICATION NUMBER: US/99/828,708
CURRENT FILING DATE: 2001-09-24
NUMBER OF SEQ ID NOS: 123
SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 17
LENGTH: 5
TYPE: PRT
ORGANISM: Homo sapiens
US-09-828-708-17

Query Match 60.0%, Score 3, DB 10, Length 5:
Best Local Similarity 100.0%, Pred. No. 2,7e-05, Indels 0,
Matches 3, Conservative 0, Mismatches 0, Gaps 0,

QY 3 SYT 5
DB 1 SYT 3

DB 1 SYT 3

RESULT 8

US-09-953-031A-8
Sequence 8, Application US/99953031A
Patent No. US20020177177A1

GENERAL INFORMATION:

APPLICANT: Bernards, Rene

APPLICANT: Zeijssen, Renate

TITLE OF INVENTION: Interaction Between Cyclin D1 and Steroid Receptor

TITLE OF INVENTION: A 101-18 Antisense Oligonucleotide Assays

FILE REFERENCE: 4248/80713

CURRENT APPLICATION NUMBER: US/99/953,031A

CURRENT FILING DATE: 2001-12-05

PRIOR APPLICATION NUMBER: US 09/402,305

PRIOR FILING DATE: 1999-04-10

NUMBER OF SEQ ID NOS: 27

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 8

LENGTH: 6

TYPE: PRT

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: DOMAIN

LOCATION: (1)...(6)

CITE INFORMATION: H 9,730, 2,116 [1] LXXIX motif

US-09-953-031A-8

Query Match 60.0%, Score 3, DB 9, Length 6:

Best Local Similarity 100.0%, Pred. No. 2,7e-05, Indels 0,

Matches 3, Conservative 0, Mismatches 0, Gaps 0,

QY 1 LES 3

DB 2 LES 4

RESULT 9

US-09-945-225-47

Sequence 47, Application US/99945225

Publication No. US2002019354A1

GENERAL INFORMATION:

APPLICANT: Chen, Ruoping

APPLICANT: Chu, Zhi Liang

APPLICANT: Dang, Huong T.

APPLICANT: Lowitz, Kevin P.

APPLICANT: Pride, Cameron

TITLE OF INVENTION: Eukaryotic And No. US2002019354A1: Polypeptide Variants of Huma

TITLE OF INVENTION: Receptors

FILE REFERENCE: AREN-0308

CURRENT APPLICATION NUMBER: US/99/945,225

CURRENT FILING DATE: 2001-11-26

PRIOR APPLICATION NUMBER: 09/470,496

PRIOR FILING DATE: 1998-10-13

PRIOR APPLICATION NUMBER: 12,000,000,00338

PRIOR FILING DATE: 1998-10-13

PRIOR APPLICATION NUMBER: 09/470,496

PRIOR FILING DATE: 2000-11-27

PRIOR APPLICATION NUMBER: 60/255,366

PRIOR FILING DATE: 2000-12-12

PRIOR APPLICATION NUMBER: 60/270,286

PRIOR FILING DATE: 2001-02-20

PRIOR APPLICATION NUMBER: 60/282,365

PRIOR FILING DATE: 2001-04-06

PRIOR APPLICATION NUMBER: 60/282,366

PRIOR FILING DATE: 2001-02-20

PRIOR APPLICATION NUMBER: 60/282,367

PRIOR FILING DATE: 2001-04-06

PRIOR APPLICATION NUMBER: 60/282,368

PRIOR FILING DATE: 2001-04-06

PRIOR APPLICATION NUMBER: 60/282,369

PRIOR FILING DATE: 2001-04-06

; PRIOR APPLICATION NUMBER: 60/260,317
 ; PRIOR FILING DATE: 2001-05-14
 ; PRIOR APPLICATION NUMBER: 60/409,206
 ; PRIOR FILING DATE: 2001-07-31
 ; NUMBER OF SEQ ID NOS: 67
 ; SOFTWARE: Patent version 3.1
 ; SEQ ID NO 47
 ; LENGTH: 6
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: No. US20020193584A1el Sequence
 US-09-945-225-47

Query Match 60.0%; Score 3; DB 9; Length 6;
 Best Local Similarity 100.0%; Pred. No. 2.7e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LES 3
 Db 2 LES 4

RESULT 10

US-10-097-175-99
 ; Sequence 99, Application US/10097175
 ; Publication No. US20030045680A1
 ; GENERAL INFORMATION:
 ; APPLICANT: JOVAL, JOHN L.
 ; APPLICANT: MUELLER, JOHN
 ; APPLICANT: OGA, VIBHA B.
 ; TITLE OF INVENTION: PEPTIDIC MODULATORS OF THE ANGIOGEN PEPTIDE
 ; FILE REFERENCE: PPI-110
 ; CURRENT APPLICATION NUMBER: US/10/097,175
 ; CURRENT FILING DATE: 2002-03-12
 ; PRIOR APPLICATION NUMBER: 60/275,240
 ; PRIOR FILING DATE: 2001-03-12
 ; PRIOR APPLICATION NUMBER: 60/7352,369
 ; PRIOR FILING DATE: 2002-01-28
 ; NUMBER OF SEQ ID NOS: 102
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 99
 ; LENGTH: 6
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Androgen Receptor Binding Polypeptides
 US-10-097-175-99

Query Match 60.0%; Score 3; DB 9; Length 6;
 Best Local Similarity 100.0%; Pred. No. 2.7e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ESY 4
 Db 2 ESY 4

RESULT 11

US-09-944-292-40
 ; Sequence 40, Application US/09/944292
 ; Patent No. US20020128433A1
 ; GENERAL INFORMATION:
 ; APPLICANT: YAO, YONG
 ; APPLICANT: XU, HONG
 ; TITLE OF INVENTION: G-ALPHA-0 PROTEIN VARIANTS AND THEIR USE IN THE
 ; TITLE OF INVENTION: ANALYSIS AND DISCOVERY OF AGONISTS AND ANTAGONISTS OF
 ; TITLE OF INVENTION: CHEMOSENSORY RECEPTORS
 ; FILE REFERENCE: 078003-0280649
 ; CURRENT APPLICATION NUMBER: US/09/944,292
 ; CURRENT FILING DATE: 2001-10-29
 ; PRIOR APPLICATION NUMBER: 60/243,770

; PRIOR FILING DATE: 2001-10-30
 ; NUMBER OF SEQ ID NOS: 42
 ; SOFTWARE: Patentin Ver. 2.1
 ; SEQ ID NO 40
 ; LENGTH: 6
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: Illustrative
 ; OTHER INFORMATION: N-terminal peptide sequence
 US-09-944-292-40

Query Match 60.0%; Score 3; DB 10; Length 6;
 Best Local Similarity 100.0%; Pred. No. 2.7e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LES 3
 Db 3 LES 5

RESULT 12

US-09-989-497-40
 ; Sequence 40, Application US/09989497
 ; Patent No. US20020143151A1
 ; GENERAL INFORMATION:
 ; APPLICANT: YAO, YONG
 ; APPLICANT: XU, HONG
 ; TITLE OF INVENTION: G-ALPHA-0 PROTEIN VARIANTS AND THEIR USE IN THE
 ; TITLE OF INVENTION: ANALYSIS AND DISCOVERY OF AGONISTS AND ANTAGONISTS OF
 ; TITLE OF INVENTION: CHEMOSENSORY RECEPTORS
 ; FILE REFERENCE: 078003-0280735
 ; CURRENT APPLICATION NUMBER: US/09/989,497
 ; CURRENT FILING DATE: 2001-11-21
 ; PRIOR APPLICATION NUMBER: 60/484,293
 ; PRIOR FILING DATE: 2001-10-29
 ; PRIOR APPLICATION NUMBER: 60/243,770
 ; PRIOR FILING DATE: 2001-10-29
 ; NUMBER OF SEQ ID NOS: 42
 ; SOFTWARE: Patentin Ver. 2.1
 ; SEQ ID NO 40
 ; LENGTH: 6
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: Illustrative
 ; OTHER INFORMATION: N-terminal peptide sequence
 US-09-989-497-40

Query Match 60.0%; Score 3; DB 10; Length 6;
 Best Local Similarity 100.0%; Pred. No. 2.7e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LES 3
 Db 3 LES 5

RESULT 13

US-09-867-852-138
 ; Sequence 138, Application US/09867852
 ; Patent No. US/98/314732A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ausubel, Frederick M.
 ; APPLICANT: Staskawicz, Brian J.
 ; APPLICANT: Brent, Andrew F.
 ; APPLICANT: Eakleek, Douglas
 ; APPLICANT: Katagiri, Fumaki
 ; APPLICANT: Kunkel, Bailata N.
 ; APPLICANT: Mindrinos, Michael N.
 ; APPLICANT: Y. Gao-Liang
 ; TITLE OF INVENTION: PPS2 GENE FAMILY, PRIMERS, PROBES, AND
 ; TITLE OF INVENTION: DETECTION METHODS

```

: FILE REFERENCE: 00786/254002
: CURRENT APPLICATION NUMBER: US/09/867,852
: CURRENT FILING DATE: 2001-05-29
: PRIOR FILING DATE: EARLIER FILING DATE: 1999-04-28
: PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/301,085
: PRIOR FILING DATE: EARLIER FILING DATE: 1994-09-02
: PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/410,912
: PRIOR FILING DATE: EARLIER FILING DATE: 1994-04-03
: PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/227,360
: NUMBER OF SEQ ID NOS: 209
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 138
: LENGTH: 6
: TYPE: PRT
: ORGANISM: Arabidopsis thaliana
US-09-867-852-138

Query Match
Best Local Similarity 60.0%; Score 3; DB 13; Length 6;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 LES 3
    |||
    3 LES 5

RESULT 14
US-10-000-273-13
: Sequence 13, Application US/10000273
: Patent No. US20020160362A1
: GENERAL INFORMATION:
: APPLICANT: Grandeurl, Andrew David John
: TITLE OF INVENTION: ROVER GENES ENCODING A GRAFT-ABLE LINE
: MOLECULES
: NUMBER OF SEQUENCES: 17
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Fish & Richardson P.C.
: STREET: 225 Franklin Street
: CITY: Boston
: STATE: MA
: COUNTRY: USA
: ZIP: 02110-2804
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Diskette
: COMPUTER: IBM Compatible
: OPERATING SYSTEM: Windows 95
: SOFTWARE: FastSeq for Windows Version 2.0b
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/10/000,273
: FILING DATE: 02-Nov-2002
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US/09/964,127
: FILING DATE: 06-NOV-1997
: ATTORNEY/AGENT INFORMATION:
: NAME: Trews, Ph.D., L. Lee
: REGISTRATION NUMBER: P-43,567
: REFERENCE/KEYWORD NUMBER: 0734,018000
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 617/542-5070
: TELEFAX: 617/542-8906
: TELEX: 200154
: INFORMATION FOR SEQ ID NO: 13:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 7 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: peptide
: SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-10-000-273-13

```

```

Query Match
Best Local Similarity 100.0%; Score 3; DB 9; Length 7;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 LES 3
    |||
Db 1 LES 3

RESULT 15
US-10-091-236-15
: Sequence 15, Application US/10001236
: Patent No. US20020168360A1
: GENERAL INFORMATION:
: APPLICANT: DINGIVAN, CHRISTINE A.
: TITLE OF INVENTION: METHODS OF PREVENTING OR TREATING INFLAMMATORY OR AUTOIMMUNE
: DISORDERS BY ADMINISTERING INTEGRIN ALPHA-V-BETA 3 ANTAGONISTS
: TITLE OF INVENTION: COMBINATION WITH OTHER PROPHYLACTIC OR THERAPEUTIC AGENTS
: FILE REFERENCE: 10271-053-999
: CURRENT APPLICATION NUMBER: US/10/091,236
: CURRENT FILING DATE: 2002-03-04
: PRIOR APPLICATION NUMBER: US 60/273,098
: PRIOR FILING DATE: 2001-03-02
: PRIOR APPLICATION NUMBER: US 60/316,321
: PRIOR FILING DATE: 2001-08-31
: NUMBER OF SEQ ID NOS: 17
: SOFTWARE: PatentIn version 3.1
: SEQ ID NO 15
: LENGTH: 7
: TYPE: PRT
: ORGANISM: Mus sp.
US-10-091-236-15

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Query Match
Best Local Similarity 60.0%; Score 3; DB 9; Length 7;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 LES 4
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Db 5 LES 7

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Search completed: April 29, 2003, 08:55:31
Job time : 10 secs

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GenCore version 5.1.4-p5-1578
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OM protein - protein search, using sw model

Run on: April 29, 2003, 08:50:15 : Search time 15,4167 Seconds
(without alignments)
9,543 Million cell updates/sec

Perfect score: 5
Sequence: 1 LESVT 5

Scoring table: CLIGO
Gapop 60.0, Gapext 60.0

Searched: 262574 seqs, 20422222 residues

Size: 0

Local number of hits satisfying chosen parameters 77191

Minimum DB seq length: 0
Maximum DB seq length: 10

Post-processing: Listing first 45 summaries

1: /cgm2_6/ptodata/1/iaa/5A-COMB-pep.*
2: /cgm2_6/ptodata/1/iaa/5B-COMB-pep.*
3: /cgm2_6/ptodata/1/iaa/5A-COMB-pep.*
4: /cgm2_6/ptodata/1/iaa/5B-COMB-pep.*
5: /cgm2_6/ptodata/1/iaa/PTUS-COMB-pep.*
6: /cgm2_6/ptodata/1/iaa/Backfiles-pep.*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3	60.0	4	4	US-09-177-249-247
2	3	60.0	5	1	US-08-385-443-5
3	3	60.0	5	1	US-08-456-840-36
4	3	60.0	5	1	US-08-170-360-11
5	3	60.0	5	1	US-08-170-360-14
6	3	60.0	5	1	US-08-302-829-8
7	3	60.0	5	1	US-08-481-840A-6
8	3	60.0	5	1	US-08-266-407A-4
9	3	60.0	5	1	US-08-403-718-8
10	3	60.0	5	1	US-08-619-462-8
11	3	60.0	5	2	US-08-892-544-36
12	3	60.0	5	3	US-09-082-837A-8
13	3	60.0	5	4	US-09-421-845-8
14	3	60.0	5	4	US-09-298-924-35
15	3	60.0	5	6	US-09-113-921-44
16	3	60.0	5	6	US-09-113-921-44
17	3	60.0	5	6	US-09-113-921-44
18	3	60.0	5	6	US-09-113-921-44
19	3	60.0	5	6	US-09-113-921-44
20	3	60.0	5	6	US-09-113-921-44
21	3	60.0	5	6	US-09-113-921-44
22	3	60.0	5	6	US-09-113-921-44
23	3	60.0	5	6	US-09-113-921-44
24	3	60.0	5	6	US-09-113-921-44
25	3	60.0	5	6	US-09-113-921-44
26	3	60.0	5	6	US-09-113-921-44
27	3	60.0	5	6	US-09-113-921-44

28 3 60.0 6 4 US-08-476-134A-33 Sequence 138, Appl
29 3 60.0 6 4 US-09-401-085-138 Sequence 138, Appl
30 3 60.0 6 4 US-09-302-3050-8 Sequence 138, Appl
31 3 60.0 6 5 PCT-US93-01669-30 Sequence 138, Appl
32 3 60.0 6 5 PCT-US93-01669-31 Sequence 138, Appl
33 3 60.0 6 5 PCT-US93-01669-31 Sequence 138, Appl
34 3 60.0 6 5 PCT-US93-01669-31 Sequence 138, Appl
35 3 60.0 6 5 PCT-US93-01669-31 Sequence 138, Appl
36 3 60.0 6 5 PCT-US93-01669-31 Sequence 138, Appl
37 3 60.0 6 5 PCT-US93-01669-31 Sequence 138, Appl
38 3 60.0 6 5 PCT-US93-01669-31 Sequence 138, Appl
39 3 60.0 6 5 PCT-US93-01669-31 Sequence 138, Appl
40 3 60.0 6 5 PCT-US93-01669-31 Sequence 138, Appl
41 3 60.0 6 5 PCT-US93-01669-31 Sequence 138, Appl
42 3 60.0 6 5 PCT-US93-01669-31 Sequence 138, Appl
43 3 60.0 6 5 PCT-US93-01669-31 Sequence 138, Appl
44 3 60.0 6 5 PCT-US93-01669-31 Sequence 138, Appl
45 3 60.0 6 5 PCT-US93-01669-31 Sequence 138, Appl

ALIGNMENTS

RESULT 1
US-09-177-249-247
Sequence 247, Application US/09/177,249
Patent No. 6229064
GENERAL INFORMATION:
APPLICANT: Fisher, Robert L.
APPLICANT: Chad, Nir
APPLICANT: Kiyosue, Tomohiro
APPLICANT: Yabuchi, Fumin
APPLICANT: Margossian, Linda
APPLICANT: Harada, John
APPLICANT: Goldberger, Robert B.
APPLICANT: The Regents of the University of California
TITLE OF INVENTION: Nucleic Acids That Control Seed and Fruit
FILE REFERENCE: 024070-08612005
CURRENT APPLICATION NUMBER: US/09/177,249
CURRENT FILING DATE: 1998-10-22
EARLIER FILING DATE: 1998-05-01
NUMBER OF SEQ ID NOS: 324
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 247
LENGTH: 4
TYPE: PRT
ORGANISM: Arabidopsis sp.
US-09-177-249-247
Query Match: 60.0% Score 3, DB 4, Length 4:
Best Local Similarity 100.0% Pred. No. 2e-05:
Matches 3: Conservative 0: Mismatches 0: Indels 0: Gaps 0:
QY 3 SYT 5
DB 1 SYT 3
RESULT 2
US-09-385-443-5
Sequence 5, Application US/08/385,443
Patent No. 5534495
GENERAL INFORMATION:
APPLICANT: FERT, CANDACE B.
APPLICANT: RUFF, MICHAEL R.
TITLE OF INVENTION: TREATMENT OF NON-HIV NEUROPATHIC
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: JULES E. GOLDBERG
STREET: 261 MADISON AVENUE

```

: CITY: NEW YORK
: STATE: NEW YORK
: COUNTRY: USA
: ZIP: 10016-2391
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent In Release #1.0, Version #1.30
: CURRENT APPLICATION NUMBER: US/08/485,443
: FILING DATE: 08-FEB-1995
: CLASSIFICATION: 514
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/567,523
: FILING DATE: 23-MAY-1993
: ATTORNEY/AGENT INFORMATION:
: NAME: GOLDBERG, JULES E.
: REGISTRATION NUMBER: 24,408
: REFERENCE/DOCKET NUMBER: ADVANCED PEPTIDES P5
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 212-986-4090
: TELEFAX: 212-818-9479
: INFORMATION FOR SEQ ID NO: 5:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 5 amino acids
: TYPE: amino acid
: STRANDEDNESS: not relevant
: TOPOLOGY: not relevant
: MOLECULE TYPE: peptide
: US-08-385-443-5

Query Match 60.0%; Score 3; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0;

QY 3 SYT 5
Db 3 SYT 5

RESULT 3
US-08-456-840-36
: Sequence 36, Application US/08456840
: Patent No. 5597908
: GENERAL INFORMATION:
: APPLICANT: Tadel; Peters, W. C.
: TITLE OF INVENTION: Immunoreactive Peptides of Apo(a)
: NUMBER OF SEQUENCES: 48
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Akzo No. 5597908el
: STREET: 1330 Piccard Drive
: CITY: Rockville
: STATE: Maryland
: COUNTRY: US
: ZIP: 20850
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent In Release #1.0, Version #1.25
: CURRENT APPLICATION NUMBER:
: FILING DATE: 01-JUN-1995
: CLASSIFICATION: 536
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/266,407
: FILING DATE: 27-JUN-1994
: APPLICATION NUMBER: US 08/172,461
: FILING DATE: 21-DEC-1993
: ATTORNEY/AGENT INFORMATION:
: NAME: Gormley, Mary E.

```

```

: REGISTRATION NUMBER: 34,409
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 301-258-5200
: TELEFAX: 301-977-0847
: INFORMATION FOR SEQ ID NO: 36:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 5 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: US-08-456-840-36

Query Match 60.0%; Score 3; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0;

QY 1 LES 4
Db 1 LES 4

RESULT 4
US-08-170-360-11
: Sequence 11, Application US/08170360
: Patent No. 5656602
: GENERAL INFORMATION:
: APPLICANT: Tseng, Albert P. S.
: APPLICANT: Inglis, Adam
: TITLE OF INVENTION: PLA2 INHIBITORY COMPOUNDS
: NUMBER OF SEQUENCES: 17
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Rothwell, Figg Ernst & Kurz
: STREET: Suite 701-E, 555 Thirteenth St., N.W.
: CITY: Washington
: STATE: D.C.
: COUNTRY: U.S.A.
: ZIP: 20004
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: OPERATING SYSTEM: IBM PC compatible
: SOFTWARE: Patent In Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/170,360
: FILING DATE: 03-MAR-1994
: CLASSIFICATION: 514
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: AU PRT/90/2,00333
: FILING DATE: 06-JUL-1992
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: AU PK 7058
: FILING DATE: 04-JUL-1991
: ATTORNEY/AGENT INFORMATION:
: NAME: Ernst, Barbara G.
: REGISTRATION NUMBER: 30,377
: REFERENCE/DOCKET NUMBER: 1871-104A
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (202)783-6040
: TELEFAX: (202)783-6031
: INFORMATION FOR SEQ ID NO: 11:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 5 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: both
: MOLECULE TYPE: peptide
: HYPOTHETICAL: NO
: ANTI-SENSE: NO
: FRAGMENT TYPE: N-terminal
: US-08-170-360-11

Query Match 60.0%; Score 3; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 2e+05;

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Matches 3: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 3 SYT 5
|||
DB 3 SYT 5

RESULT 5

US-08-170-360-14
: Sequence 14, Application US/08170360
: Patent No. 5656602
: GENERAL INFORMATION:
: APPLICANT: Tsen, Albert P. S.
: APPLICANT: Ingilis, Adam
: TITLE OF INVENTION: PLA2 INHIBITORY COMPOUNDS
: NUMBER OF SEQUENCES: 17
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Rothwell, Figg Ernst & Kurz
: STREET: Suite 701-F, 545 Thirteenth St., N.W.
: CITY: Washington
: STATE: D.C.
: COUNTRY: U.S.A.
: ZIP: 20004

: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC DOS/MS-DOS
: SOFTWARE: Patent Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US 08/170,360
: FILING DATE: 03-MAR-1994
: CLASSIFICATION: 514
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: AU PCI/AUG2/56333
: FILING DATE: 06-JUL-1992
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: AU PK 7058
: FILING DATE: 04-JUL-1991
: ATTORNEY/AGENT INFORMATION:
: NAME: Ernst, Barbara G.
: REGISTRATION NUMBER: 40,377
: REFERENCE/DOCKET NUMBER: 1871-104A
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (202) 793-6040
: TELEFAX: (202) 793-6011
: INFORMATION FOR SEQ ID NO: 14:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 5 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: both
: MOLECULE TYPE: Peptide
: HYPOTHETICAL: NO
: ANTI-SENSE: NO
: FRAGMENT TYPE: N-terminal
US-08-170-360-14

Query Match 60.0% Score 3: DB 1 Length 5;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 3: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 2 ESY 4
|||
DB 2 ESY 4

RESULT 6

US-08-302-829-8
: Sequence 8, Application US/08302829
: Patent No. 5756440
: GENERAL INFORMATION:
: APPLICANT: ANDERSEN, Anders J
: APPLICANT: ASION, Roger

: APPLICANT: CARLEN, Peter L
: APPLICANT: DOOB, Renelope R
: APPLICANT: MacFADDEN, Douglas K
: APPLICANT: PHIPPS, David J
: APPLICANT: RATHJEN, Deborah
: APPLICANT: WIDMER, Fred
: TITLE OF INVENTION: Peptide T and Related Peptides in the
: TITLE OF INVENTION: Treatment of Inflammation, Including Multiple Sclerosis
: NUMBER OF SEQUENCES: 11
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: BANNER & ALLEGRETTI, LTD.
: STREET: 10 S Wacker Drive
: CITY: Chicago
: STATE: Illinois
: COUNTRY: USA
: ZIP: 60606

: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC DOS/MS-DOS
: SOFTWARE: Patent Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US 08/090,809
: FILING DATE: 29-MAR-1993
: CLASSIFICATION: 514
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/955,006/49
: FILING DATE: 29-MAR-1993
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/937,674
: FILING DATE: 09-DEC-1992
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/915,118
: FILING DATE: 17-JUL-1992
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/845,792
: FILING DATE: 14-MAY-1992
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/809,932
: FILING DATE: 27-MAR-1992
: ATTORNEY/AGENT INFORMATION:
: NAME: McDowell, John J
: REGISTRATION NUMBER: 26949
: REFERENCE/DOCKET NUMBER: 91,372
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 312-715-1000
: TELEFAX: 312-715-1234
: INFORMATION FOR SEQ ID NO: 8:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 5 amino acids
: TYPE: amino acid
: STRANDEDNESS: not relevant
: TOPOLOGY: both
: MOLECULE TYPE: peptide
US-08-302-829-8

Query Match 60.0% Score 3: DB 1 Length 5;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 3: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 3 SYT 5
|||
DB 3 SYT 5

RESULT 7

US-08-481-840A-6
: Sequence 6, Application US/08481840A
: Patent No. 5753406
: GENERAL INFORMATION:
: APPLICANT: PEDERSEN, Ove
: APPLICANT: MACFADDEN, D.
: TITLE OF INVENTION: Peptides for Treatment

```

1  NUMBER OF SEQUENCES: 7
2  CORRESPONDENCE ADDRESS:
3  ADDRESSEE: Banner & Allegretti, Ltd.
4  STREET: 10 South Wacker Drive
5  CITY: Chicago
6  STATE: Illinois
7  COUNTRY: USA
8  ZIP: 60606
9  COMPUTER READABLE FORM:
10 MEDIUM TYPE: Floppy disk, 3.50 inch
11 COMPUTER: IBM PC compatible
12 OPERATING SYSTEM: MS-DOS
13 SOFTWARE: WordPerfect 6.1
14 CURRENT APPLICATION DATA:
15 APPLICATION NUMBER: US/08/481,840A
16 FILING DATE: 07-JUN-1995
17 CLASSIFICATION: 514
18 PRIOR APPLICATION DATA:
19 APPLICATION NUMBER: 08/107,777
20 FILING DATE: 24-NOV-1993
21 ATTORNEY/AGENT INFORMATION:
22 NAME: Iwanicki, John P.
23 REGISTRATION NUMBER: 34,628
24 REFERENCE/DOCKET NUMBER: 93,741-A
25 TELECOMMUNICATION INFORMATION:
26 TELEPHONE: 617-345-9100
27 TELEFAX: 617-345-9111
28 INFORMATION FOR SEQ ID NO. 6:
29 SEQUENCE CHARACTERISTICS:
30 LENGTH: 5 amino acids
31 TYPE: amino acid
32 STRANDEDNESS:
33 TOPOLOGY: Linear
34 MOLECULE TYPE: peptide
35 US-08-481-840A-6
36
37 Query Match 60.0%; Score 3; DB 1; Length 5;
38 Best Local Similarity 100.0%; Pred. No. 2e+05;
39 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
40
41 QY 3 SYT 5
42 III
43 DB 3 SYT 5
44
45 RESULT 8
46 US-08-266-407A-36
47 Sequence 36, Application US/08266407A
48 Patent No. 5786156
49 GENERAL INFORMATION:
50 APPLICANT: Tadel-Peters, W. C.
51 APPLICANT: Butler, Sandra M.
52 TITLE OF INVENTION: Immunoreactive Peptides of Apo(a)
53 NUMBER OF SEQUENCES: 48
54 CORRESPONDENCE ADDRESS:
55 ADDRESSEE: Akzo NO. 5786156el
56 STREET: 1330 Piccard Drive
57 CITY: Rockville
58 STATE: Maryland
59 COUNTRY: US
60 ZIP: 20850
61 COMPUTER READABLE FORM:
62 MEDIUM TYPE: Floppy disk
63 COMPUTER: IBM PC compatible
64 OPERATING SYSTEM: PC-DOS/MS-DOS
65 SOFTWARE: PatentIn Release #1.0, Version #1.25
66 CURRENT APPLICATION DATA:
67 APPLICATION NUMBER: US/08/266,407A
68 FILING DATE: 27-JUN-1994
69 CLASSIFICATION: 435
70 PRIOR APPLICATION DATA:
71 APPLICATION NUMBER: US 08/172,461
72 FILING DATE: 21-DEC-1993

```

```

1  ATTORNEY/AGENT INFORMATION:
2  NAME: Gormley, Mary E.
3  REGISTRATION NUMBER: 34,409
4  TELECOMMUNICATION INFORMATION:
5  TELEPHONE: 301-258-5200
6  TELEFAX: 301-977-0847
7  INFORMATION FOR SEQ ID NO: 36:
8  SEQUENCE CHARACTERISTICS:
9  LENGTH: 5 amino acids
10 TYPE: amino acid
11 TOPOLOGY: linear
12 MOLECULE TYPE: protein
13 US-08-266-407A-36
14
15 Query Match 60.0%; Score 3; DB 1; Length 5;
16 Best Local Similarity 100.0%; Pred. No. 2e+05;
17 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
18
19 QY 1 LES 3
20 III
21 DB 1 LES 3
22
23 RESULT 9
24 US-08-403-718-8
25 Sequence 8, Application US/08403718
26 Patent No. 5795858
27 GENERAL INFORMATION:
28 APPLICANT: MICHAELIS, JURGEN
29 APPLICANT: SLEIGH, MERILYN J.
30 TITLE OF INVENTION: TREATMENT OR PREVENTION OF CROHN'S
31 TITLE OF INVENTION: DISEASE AND/OR ULCERATIVE COLITIS
32 NUMBER OF SEQUENCES: 8
33 CORRESPONDENCE ADDRESS:
34 ADDRESSEE: NIXON & VANDERHYE P.C.
35 STREET: 1100 NORTH GLEBE ROAD
36 CITY: ARLINGTON
37 STATE: VIRGINIA
38 COUNTRY: U.S.A.
39 ZIP: 22201-4714
40 COMPUTER READABLE FORM:
41 MEDIUM TYPE: Floppy disk
42 COMPUTER: IBM PC compatible
43 OPERATING SYSTEM: PC-DOS/MS-DOS
44 SOFTWARE: PatentIn Release #1.0, Version #1.30
45 CURRENT APPLICATION DATA:
46 APPLICATION NUMBER: US/08/403,718
47 FILING DATE: 31-MAR-1995
48 CLASSIFICATION: 514
49 ATTORNEY/AGENT INFORMATION:
50 NAME: MITCHARD, LEONARD C.
51 REGISTRATION NUMBER: 29,009
52 REFERENCE/DOCKET NUMBER: 47-74
53 TELECOMMUNICATION INFORMATION:
54 TELEPHONE: (703) 816-4000
55 TELEFAX: (704) 816-4100
56 INFORMATION FOR SEQ ID NO: -8:
57 SEQUENCE CHARACTERISTICS:
58 LENGTH: 5 amino acids
59 TYPE: amino acid
60 STRANDEDNESS:
61 TOPOLOGY: linear
62 MOLECULE TYPE: peptide
63 US-08-403-718-8
64
65 Query Match 60.0%; Score 3; DB 1; Length 5;
66 Best Local Similarity 100.0%; Pred. No. 2e+05;
67 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
68
69 QY 3 SYT 5
70 III
71 DB 3 SYT 5

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```

RESULT 10
US-08-619-462-8
: Sequence 8, Application US/08619462
: Patent No. 5798335
: GENERAL INFORMATION:
: APPLICANT: MICHAELIS, JURGEN
: APPLICANT: T-197, Timothy Elliot
: TITLE OF INVENTION: METHOD FOR THE TREATMENT OF PREVENTION OF
: TITLE OF INVENTION: EYEMA, DERMATITIS
: NUMBER OF SEQUENCES: 8
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: NIXON & VANDEPHEVE P.C.
: STREET: 1100 NORTH CLERE ROAD
: CITY: ARLINGTON
: STATE: VIRGINIA
: COUNTRY: U.S.A.
: ZIP: 22201-4734
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent In Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US-08-619-462
: FILING DATE: 07-MAY-1996
: CLASSIFICATION: 514
: ATTORNEY/AGENT INFORMATION:
: NAME: MITCHELL, LEONARD C.
: REGISTRATION NUMBER: 29,009
: REFERENCE/DOCKET NUMBER: 47-84
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (703) 816-4000
: TELEFAX: (703) 816-4100
: INFORMATION FOR SEQ ID NO: 8:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 5 amino acids
: TYPE: amino acid
: STRANDEDNESS:
: TOPOLOGY: linear
: MOLECULE TYPE: peptide
US-08-619-462-8

Query Match 60.0% Score 3; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 2e+00
Matches 3; Conservative 0; Mismatches 0; Indels 0;

QY 3 SYT 5
   |||
   3 SYT 5

RESULT 11
US-08-892-544-36
: Sequence 36, Application US/08892544
: Patent No. 5874544
: GENERAL INFORMATION:
: APPLICANT: Taddel-Peters, W. C.
: APPLICANT: Butler, Sandra M.
: TITLE OF INVENTION: Immunoreactive Peptides of Apo(a)
: NUMBER OF SEQUENCES: 48
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Apt. No. 5974544c1
: STREET: 1370 Piccard Drive
: CITY: Rockville
: STATE: Maryland
: COUNTRY: US
: ZIP: 20850
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent In Release #1.0, Version #1.25

```

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: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/992,544
: FILING DATE:
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US/08/286,407
: FILING DATE: 27-JUN-1994
: APPLICATION NUMBER: US/08/272,461
: FILING DATE: 21-DEC-1993
: ATTORNEY/AGENT INFORMATION:
: NAME: Gormley, Mary E.
: REGISTRATION NUMBER: 34,409
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 301-258-5200
: TELEFAX: 301-977-0847
: INFORMATION FOR SEQ ID NO: 36:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 5 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
US-08-892-544-36

Query Match 60.0% Score 3; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0;

QY 1 LES 3
   |||
   1 LES 3

RESULT 12
US-09-082-837A-9
: Sequence 8, Application US/09082837A
: Patent No. 6011014
: GENERAL INFORMATION:
: APPLICANT: ANDERSEN, Anders J.
: APPLICANT: ASTON, Roger
: APPLICANT: CARLEN, Peter L.
: APPLICANT: DOOB, Penelope K.
: APPLICANT: MAGFADDAN, Douglas K.
: APPLICANT: PHIPPS, David J.
: APPLICANT: RATHJEN, Deborah
: APPLICANT: WIDMER, Fred
: TITLE OF INVENTION: Peptide T and Related Peptides in the Treatment of
: TITLE OF INVENTION: Inflammation, Including Multiple Sclerosis
: NUMBER OF SEQUENCES: 11
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: BANNER & WITCOFF, LTD.
: STREET: 10 S. Wacker Drive
: CITY: Chicago
: STATE: Illinois
: COUNTRY: USA
: ZIP: 60606
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent In Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/082,837A
: FILING DATE: 21-JUN-1998
: CLASSIFICATION: 514
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US/08/202,929
: FILING DATE: 29-MAR-1993
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: WO/97/046,000/649
: FILING DATE: 29-MAR-1993
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US/07/987,674
: FILING DATE: 09-DEC-1992

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Sequence 35, Application US/09/298924
Patent No. 6391595
GENERAL INFORMATION:
APPLICANT: KATO, Masaru
MIURA, Yutaka
KETTOKU, Masako
IWAMATSU, Akihiro
KOBAYASHI, Kazuo
KOMEDA, Toshihiro
TITLE OF INVENTION: NOVEL TRANSFERASE AND AMYLASE, PROCESS
FOR PROTECTING THE ENZYMES, USE THEREOF, AND GENE CODING
FOR THE SAME
NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: 08/750,569
FILING DATE: 26-Apr-1999
CLASSIFICATION: <unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/750,569
FILING DATE: <unknown>
APPLICATION NUMBER: JP 7-120673
FILING DATE: 21-Apr-1995
APPLICATION NUMBER: JP 6-311185
FILING DATE: 21-Nov-1994
APPLICATION NUMBER: JP 6-286917
FILING DATE: 21-Nov-1994
APPLICATION NUMBER: JP 6-290394
FILING DATE: 31-Oct-1994
APPLICATION NUMBER: JP 6-194223
FILING DATE: 18-Aug-1994
APPLICATION NUMBER: JP 6-133354
FILING DATE: 16-Jun-1994
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/AGENT NUMBER: 49441/110
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 35:
US-09-298-924-35
Query Match 60.0% Score 3; DB 4; Length 5;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LES 3
DB 3 LES 5
RESULT 15
5276016-4
Patent No. 5276016

Prior Application Data:
Application Number: US 07/915,118
Filing Date: 17-Jul-1992
Prior Application Data:
Application Number: DK 645/92
Filing Date: 14-May-1992
Prior Application Data:
Application Number: US 07/858,832
Filing Date: 27-Mar-1992
Attorney/Agent Information:
Name: Drekhoff, W. Dennis
Registration Number: 27193
Reference/Pocket Number: 94,772-A
Telecommunication Information:
Telephone: 312-715-1000
Telefax: 312-715-1234
Information for Seq ID No: 8:
Sequence Characteristics:
Length: 5 amino acids
Type: amino acid
Strandedness: not relevant
Topology: both
Molecule Type: peptide
US-09-082-837A-8
Query Match 60.0% Score 3; DB 3; Length 5;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3 SYT 5
DB 3 SYT 5
RESULT 13
US-09-421-845-8
Sequence 8, Application US/09421845
Patent No. 6265374
GENERAL INFORMATION:
APPLICANT: Jorgensen
APPLICANT: Aston
APPLICANT: Carlen
APPLICANT: Deeb
APPLICANT: MacFadden
APPLICANT: Phipps
APPLICANT: Rathjen
APPLICANT: Wadmer
TITLE OF INVENTION: Peptide T and Related Peptides In the Treatment of
Inflammation, Including Multiple Sclerosis.
FILE REFERENCE: Peptide T Inflammation
CURRENT APPLICATION NUMBER: US/09/421,845
CURRENT FILING DATE: 1999-10-20
PRIOR APPLICATION NUMBER: 09/082,837
PRIOR FILING DATE: 1998-05-21
NUMBER OF SEQ ID NOS: 11
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 8
LENGTH: 5
TYPE: PRT
ORGANISM: Homo sapiens
US-09-421-845-8
Query Match 60.0% Score 3; DB 4; Length 5;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3 SYT 5
DB 3 SYT 5
RESULT 14
US-09-298-924-35

APPLICANT: PERT, CANDACE B.; RUFF, WILLIAM F.
FARRAR, WILLIAM L.
TITLE OF INVENTION: SMALL PEPTIDES WHICH INHIBIT
BINDING TO T-4 RECEPTORS AND ACT AS IMMUNOGENS
NUMBER OF SEQUENCES: 19
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US 07,669,616
FILING DATE: 16-AUG-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 314,507
FILING DATE: 15-FEB-1989
APPLICATION NUMBER: 487,148
FILING DATE: 11-MAY-1987
APPLICATION NUMBER: 878,585
FILING DATE: 26-JUN-1986
APPLICATION NUMBER: 869,919
FILING DATE: 03-JUN-1986
SEQ ID NO: 4
LENGTH: 5
526016-4

Seq Match 60.0%; Score 3; DB 6; Length 5;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 3; Conservative 0; Mismatches 0; Gaps 3;

QY 3 SYT 5
BB 3 SYT 5

Search completed: April 29, 2003, 09:55:02
Job time: 17.4167 secs

GenCore version 5.1.4.10.4578
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OM protein - protein search, using sw model

Run on: April 29, 2003, 08:50:15 : Search time 21 5833 Seconds
(without alignments)
9.543 Million cell updates/sec

Title: US-09-647-749A-2

Perfect score: 7
Sequence: 1 IKEYETS 7

Scoring table: CLUSTAL Gapop 50.0 : Gapext 60.0

Searched: 262574 seqs, 29422922 residues

Word size : 0

Total number of hits satisfying chosen parameters: 77191

Minimum DB seq length: 0
Maximum DB seq length: 10

Post-processing: listing first 45 summaries

Database : Issued Patents AA*

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4: /gmo-6/prodata/1/aa/5D-CMB.pep*
5: /gmo-6/prodata/1/aa/5E-CMB.pep*
6: /gmo-6/prodata/1/aa/5F-CMB.pep*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	4	57.1	9	4	US-09-187-859-2791
2	4	57.1	9	5	PCT-US95-16415-34
3	4	57.1	10	4	US-09-187-859-2791
4	3	42.9	4	1	US-08-416-007-3
5	3	42.9	4	2	US-08-475-251-3
6	3	42.9	5	1	US-08-244-546-3
7	3	42.9	5	1	US-08-737-757-3
8	3	42.9	5	2	US-08-574-959A-11
9	3	42.9	5	2	US-08-442-016-7
10	3	42.9	5	2	US-08-684-594-7
11	3	42.9	5	3	US-08-593-740-42
12	3	42.9	5	3	US-08-488-141A-71
13	3	42.9	5	3	US-08-469-411A-71
14	3	42.9	5	4	US-08-591-832-24
15	3	42.9	5	4	US-08-109-879-47
16	3	42.9	5	4	US-09-357-014-11
17	3	42.9	5	4	US-09-267-929-11
18	3	42.9	4	1	US-09-611-451-24
19	3	42.9	5	4	US-08-306-842A-54
20	3	42.9	5	5	PCT-US95-13794-71
21	3	42.9	5	5	PCT-US95-13794-71
22	4	42.9	6	1	US-08-297-731-4
23	3	42.9	6	1	US-08-290-448A-41
24	3	42.9	6	1	US-08-290-448A-41
25	3	42.9	6	1	US-08-175-069A-41
26	3	42.9	6	2	US-08-528-523-4
27	3	42.9	6	4	US-08-893-654B-15

28 3 42.9 6 4 US-09-243-271-28
29 3 42.9 6 4 US-09-623-618B-6
30 3 42.9 6 4 US-08-471-979A-41
31 3 42.9 6 4 US-08-464-000-41
32 3 42.9 6 4 US-09-556-605-52
33 3 42.9 6 5 PCT-US95-10793-4
34 3 42.9 6 6 518642-7
35 3 42.9 6 6 510657-19
36 3 42.9 7 1 US-08-137-614A-31
37 3 42.9 7 1 US-09-297-731-5
38 3 42.9 7 1 US-07-942-245-500
39 3 42.9 7 2 US-08-317-310A-18
40 3 42.9 7 4 US-09-623-618B-7
41 3 42.9 7 4 US-09-187-859-457
42 3 42.9 7 4 US-09-187-859-4047
43 3 42.9 7 4 US-09-556-605-51
44 3 42.9 7 5 PCT-US95-10793-5
45 3 42.9 7 5 PCT-US95-14041-18

ALIGNMENTS

RESULT 1
US-09-187-859-2791
Sequence 2791, Application US/09187859A
Patent No. 6358520

GENERAL INFORMATION:
APPLICANT: Blaschuk, Orest W.
TITLE OF INVENTION: COMPLEXES AND METHODS FOR MODULATING NON-CLASSICAL
TITLE OF INVENTION: CACHEMIN-MEDIATED FUNCTIONS
FILE REFERENCE: 1009 4701
CURRENT APPLICATION NUMBER: 09-187-859A
CURRENT FILING DATE: 1998-11-06
PCT REFERENCE: PCT/US 95/4952
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO: 2791
LENGTH: 9
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Representative cyclic modulation agent based on
OTHER INFORMATION: Protocadherin cell adhesion recognition sequence
US-09-187-859-2791

Query Match 57.1% Score 4; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 3 EYFT 5
Db 1 EYFT 4

RESULT 2

PCT-US95-16415-34

Sequence 34, Application US/09516415

GENERAL INFORMATION:
APPLICANT: The Scripps Research Institute
TITLE OF INVENTION: IN VIVO ACTIVATION OF TWEET-SPECIFIC
TITLE OF INVENTION: CYTOTOXIC T CELLS
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESS: The Scripps Research Institute
STREET: 10550 North Torrey Pines Road, IPC-8
CITY: La Jolla
STATE: California
COUNTRY: US
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.5
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: PCT/US95/16415
 FILING DATE: 13-DEC-1995
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/355,558
 FILING DATE: 14-DEC-1994
 ATTORNEY/AGENT INFORMATION:
 NAME: Logan, April C.
 REGISTRATION NUMBER: 33,950
 REFERENCE/DOCKET NUMBER: 433 IPC
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (619) 554-2937
 TELEFAX: (619) 554-6412
 INFORMATION FOR SEQ ID NO: 34:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 4 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: heptade
 PCT-US95-16415-34

Query Match 57.1% Score 4 DB 4 Length 10
 Best Local Similarity 100.0% Pred. No. 2e-05
 Matches 4: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 EYFT 6
 DB 5 EYFT 8

RESULT 3
 US-09-187-859-2792
 Sequence 2792, Application US/09187859A
 Patent No. 6358920
 GENERAL INFORMATION:
 APPLICANT: Blaschuk, Orest W.
 APPLICANT: Gour, Barbara J.
 TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
 TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS
 FILE REFERENCE: 100086.407C1
 CURRENT APPLICATION NUMBER: US/09/187.859A
 CURRENT FILING DATE: 1998-11-06
 NUMBER OF SEQ ID NOS: 4052
 SOFTWARE: Patent In Ver. 2.0
 SEQ ID NO 2792
 LENGTH: 10
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Representative cyclic adhesion protein based on
 OTHER INFORMATION: Protocadherin cell adhesion recognition sequence
 US-09-187-859-2792

Query Match 57.1% Score 4 DB 4 Length 10
 Best Local Similarity 100.0% Pred. No. 3e-05
 Matches 4: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 EYFT 6
 DB 1 EYFT 4

RESULT 4
 US-08-416-007-3
 Sequence 3, Application US/08416007
 Patent No. 5693679
 GENERAL INFORMATION:
 APPLICANT: Vincent, Jean-Pierre
 APPLICANT: Gaudriault, Georges

TITLE OF INVENTION: FLUORESCENT SOMATOSTATIN
 NUMBER OF SEQUENCES: 5
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Fish & Richardson P.C.
 STREET: 225 Franklin Street
 CITY: Boston
 STATE: MA
 COUNTRY: USA
 ZIP: 02110-2804
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/416.007
 FILING DATE: 04-APR-1995
 CLASSIFICATION: 530
 ATTORNEY/AGENT INFORMATION:
 NAME: Clark, Paul T.
 REGISTRATION NUMBER: 30,162
 REFERENCE/DOCKET NUMBER: 06942/0009001
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 617/542-5070
 TELEFAX: 617/542-8906
 TELEX: 200154
 INFORMATION FOR SEQ ID NO: 3:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 4 amino acids
 TYPE: amino acid
 STRANDEDNESS: not relevant
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-416-007-3

Query Match 42.9% Score 3 DB 1 Length 4
 Best Local Similarity 100.0% Pred. No. 2e-05
 Matches 3: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 FTS 7
 DB 1 FTS 3

RESULT 5
 US-08-475-751-4
 Sequence 3, Application US/08475751
 Patent No. 5824772
 GENERAL INFORMATION:
 APPLICANT: Vincent, Jean-Pierre
 APPLICANT: Gaudriault, Georges
 TITLE OF INVENTION: FLUORESCENT SOMATOSTATIN
 NUMBER OF SEQUENCES: 5
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Clark & Elbing LLP
 STREET: 585 Commercial Street
 CITY: Boston
 STATE: MA
 COUNTRY: USA
 ZIP: 02109-1024
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/475.751
 FILING DATE: 07-JUN-1995
 CLASSIFICATION: 530
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/416.007
 FILING DATE: 04-APR-1995

```

; ATTORNEY/AGENT INFORMATION:
; NAME: Clark, Paul T.
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 06942/004001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/723-4123
; TELEFAX: 617/723-8962
; TELEX:
;
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-475-751-3

Query Match 42.9%; Score 3; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 2e+05; 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 FTS 7
Ib 1 FTS 3

RESULT 6
US-08-244-646-3
; Sequence 3, Application US/0824463
; Patent No. 5744692
; GENERAL INFORMATION:
; APPLICANT: Ceryone, Felice
; APPLICANT: De Lorenzo, Giulia
; APPLICANT: Salvi, Giovanni
; APPLICANT: Albersheim, Peter
; APPLICANT: Darvill, Alan
; APPLICANT: Bergmann, Carl
; TITLE OF INVENTION: Nucleotide Sequences Coding An
; TITLE OF INVENTION: Endopolygalacturonase Inhibitor
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sally A. Sullivan
; STREET: 5470 Manhattan Circle Suite 201
; CITY: Boulder
; STATE: CO
; COUNTRY: US
; ZIP: 80303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US 08 144 647
; FILING DATE: 06-JUN-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: IT 91A 000915
; FILING DATE: 06-DEC-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/IT/00158
; FILING DATE: 04-DEC-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Sullivan, Sally A.
; REGISTRATION NUMBER: 32,054
; REFERENCE/DOCKET NUMBER: 19-94
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (303)499-8090
; TELEFAX: (303)499-8090
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid

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; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Plasmodium vulgare
; STRAIN: Pinto
; US-08-244-646-3

Query Match 42.9%; Score 3; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 2e+05; 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 FTS 7
Db 2 FTS 4

RESULT 7
US-08-737-757-3
; Sequence 3, Application US/08737757
; Patent No. 5783413
; GENERAL INFORMATION:
; APPLICANT: Pedersen, John
; APPLICANT: Lauritzen, Conni
; APPLICANT: Madsen, Mads Thorup
; TITLE OF INVENTION: An enzymatic process for
; TITLE OF INVENTION: Producing a desired protein from an amino terminally extend
; TITLE OF INVENTION: protein
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Darby & Darby, PC
; STREET: 805 Third Avenue - 27th floor
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10022-7513
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/737,757
; FILING DATE: 05-FEB-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Gogoris, Adda C
; REGISTRATION NUMBER: 29,714
; REFERENCE/DOCKET NUMBER: 4-97, 06596
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-527-7700
; TELEFAX: 212-751-6237
; TELEX:
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-737-757-3

Query Match 42.9%; Score 3; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 2e+05; 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 FTS 7
Ib 1 FTS 3

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```

Lb      3 FTS 5
RESULT 8
US-08-574-959A-11
; Sequence 11, Application US/0857495A
; Patent No. 5962224
; GENERAL INFORMATION:
; APPLICANT: Jaekyoon Shin, Insil Joong, Rahn, K. Vadlamudi
; APPLICANT: and Jack L. Strominger
; TITLE OF INVENTION: P2 POLYPEPTIDES, RELATED POLYPEPTIDES
; TITLE OF INVENTION: AND USES THEREFOR
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street, Suite 510
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08-574-959A
; FILING DATE: 19-DEC-95
; ATTORNEY/AGENT INFORMATION:
; NAME: Mandragoras, Amy E.
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: IPN-008
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)227-5941
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
US-08-574-959A-11

Query Match      42.9%  Score 3:  DB 2:  Length 5:
Best Local Similarity 100.0%:  Prod. No. 2e-05:
Matches      3:  Conservative      0:  Mismatches      0:  Indels      0:  Gaps      0:

QY      1 IKE 3
      |||
Db      3 IKE 5

RESULT 9
US-08-432-016-7
; Sequence 7, Application US/08432016
; Patent No. 5968768
; GENERAL INFORMATION:
; APPLICANT: HAYNES, BARTON F.
; APPLICANT: ARUFFO, ALEJANDRO
; APPLICANT: PATEL, DRAVALKUMAR
; APPLICANT: BOWEN, MICHAEL A.
; APPLICANT: MARQUARDT, HANS
; TITLE OF INVENTION: CD6 LIGAND
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHYE P.C.
; STREET: 1100 NORTH GLENE ROAD
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: U.S.A.
; ZIP: 22201-4714
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/684,594
; FILING DATE: 18-JUL-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; PRIOR APPLICATION NUMBER: US 08/432,016
; FILING DATE: 01-MAY-1995
; PRIOR APPLICATION DATA:
; PRIOR APPLICATION NUMBER: US 08/433,350
; FILING DATE: 02-NOV-1994
; COMPUTER READABLE FORM:

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PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/143,903
 FILING DATE: 02-NOV-1993
 ATTORNEY/AGENT INFORMATION:
 NAME: WILSON, MAPY J
 REGISTRATION NUMBER: 32,955
 REFERENCE/DOCKET NUMBER: 1579-112
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (703) 816-4000
 TELEFAX: (703) 816-4100
 INFORMATION FOR SEQ ID NO: 7:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 5 amino acids
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-584-594-7

Query Match 42.9% Score 3: DB 3: Length 5:
 Best Local Similarity 100.0%; Pred. No. 2e-05;
 Matches 3: Conservative 0: Mismatches 0: Indels 0:

QY 1 IKE 3
 Db 1 IKE 3

RESULT 11
 US-08-582-740-42
 Sequence 42, Application US/08582740
 Patent No. 6037324
 GENERAL INFORMATION:
 APPLICANT: Schwender, Charles F.
 APPLICANT: Shroff, Hitesh N.
 TITLE OF INVENTION: Inhibitors of MadCAM-1-Mediated
 TITLE OF INVENTION: Interactions and Methods of Use Therefor
 NUMBER OF SEQUENCES: 70
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Hamilton Brook Smith & P-200-14- P
 STREET: Two Militia Drive
 CITY: Lexington
 STATE: Massachusetts
 COUNTRY: USA
 ZIP: 02173
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-OS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US-08-582-740
 FILING DATE: 04-JAN-1996
 CLASSIFICATION: 514
 ATTORNEY/AGENT INFORMATION:
 NAME: Brook, David B.
 REGISTRATION NUMBER: 22,592
 REFERENCE/DOCKET NUMBER: LKS95-12
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (617) 861-6240
 TELEFAX: (617) 861-9540
 INFORMATION FOR SEQ ID NO: 42:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 5 amino acids
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 FEATURE:
 NAME/KEY: Modified-site
 LOCATION: 1
 OTHER INFORMATION: /label=modified aa
 OTHER INFORMATION: /note="Ac - Leucine"

FEATURE:
 NAME/KEY: Modified-site
 LOCATION: 5
 OTHER INFORMATION: /label=modified aa
 OTHER INFORMATION: /note="Leucine - RH2"
 US-08-582-740-42

Query Match 42.9% Score 3: DB 3: Length 5:
 Best Local Similarity 100.0%; Pred. No. 2e-05;
 Matches 4: Conservative 0: Mismatches 0: Indels 0:

QY 5 FTS 7
 Db 2 FTS 4

RESULT 12
 US-08-469-141A-20
 Sequence 20, Application US/08469141A
 Patent No. 6124107
 GENERAL INFORMATION:
 APPLICANT: HOFFER, RICHARD A.
 APPLICANT: DAVIES, D.T. PHILIP
 APPLICANT: DAHLGREN, MARY E.
 APPLICANT: RAGER, JOSHUA S.
 APPLICANT: HOMES, JOHN L.
 TITLE OF INVENTION: ASSAY FOR MARKER OF HUMAN
 TITLE OF INVENTION: POLYMERHORMONAL LYMPHOCYTE ELASTASE ACTIVITY
 NUMBER OF SEQUENCES: 71
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: RE, CHRISTINE E. CARTY
 STREET: 126 E. LINCOLN AVENUE, P.O. BOX 2000
 CITY: RARITON
 STATE: NEW JERSEY
 COUNTRY: USA
 ZIP: 07065-0907
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-OS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08469141A
 FILING DATE: 06-JUN-1995
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: CARTY, CHRISTINE E.
 REGISTRATION NUMBER: 36,099
 REFERENCE/DOCKET NUMBER: 174611B
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (908)-594-5734
 TELEFAX: (908)-594-4720
 INFORMATION FOR SEQ ID NO: 20:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 5 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 FRAGMENT TYPE: internal
 US-08-469-141A-20

Query Match 42.9% Score 3: DB 3: Length 5:
 Best Local Similarity 100.0%; Pred. No. 2e-05;
 Matches 3: Conservative 0: Mismatches 0: Indels 0:

QY 5 FTS 7
 Db 1 FTS 3

RESULT 14
US-08-469-141A-71
Sequence 71, Application US/08469141A
Patent No. 6124107
GENERAL INFORMATION:
APPLICANT: MUMFORD, RICHARD A.
APPLICANT: DAVIES, D.F. PHILIP
APPLICANT: DAHLGREN, MARY E.
APPLICANT: BOGER, JOSHUA S.
APPLICANT: HOMES, JOHN L.
TITLE OF INVENTION: ASSAY FOR MARKER OF HUMAN
POLYMORPHONUCLEAR LEUKOCYTE ELASTASE ACTIVITY
NUMBER OF SEQUENCES: 71
CORRESPONDENCE ADDRESS:
ADDRESSEE: DR. CHRISTINE E. CARTY
STREET: 126 E. LINCOLN AVENUE, P.O. BOX 2009
CITY: RAHWAY
STATE: NEW JERSEY
COUNTRY: USA
ZIP: 07065-0907
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/469/141A
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: CARTY, CHRISTINE E.
REGISTRATION NUMBER: 36,099
REFERENCE/DOCKET NUMBER: 174611B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908)-594-6734
TELEFAX: (908)-594-4720
INFORMATION FOR SEQ ID NO: 71:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: internal
US-08-469-141A-71
Query Match 42.9%, Score 3, DB 3, Length 5:
Best Local Similarity 100.0%, Pred. No. 2e+05:
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0:
QY 5 FTS 7
DB 1 FTS 3
RESULT 14
US-08-591-632-24
Sequence 24, Application US/08591632
Patent No. 6261558
GENERAL INFORMATION:
APPLICANT: Barbas, Carlos F.
APPLICANT: Burton, Dennis R.
APPLICANT: Leifer, Richard A.
TITLE OF INVENTION: SYNTHETIC HUMAN NEUTRALIZING MONOCLONAL
ANTIBODIES TO HUMAN IMMUNODEFICIENCY VIRUS
NUMBER OF SEQUENCES: 92
CORRESPONDENCE ADDRESS:
ADDRESSEE: The Scripps Research Institute, Office of
ADDRESSEE: Patent Counsel
STREET: 10550 No. 6261558th Torrey Pines Road, TPC 8
CITY: La Jolla

STATE: CA
COUNTRY: USA
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/691/632
FILING DATE: 19-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/211907
FILING DATE: 19-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/208,841
FILING DATE: 19-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/233,619
FILING DATE: 26-APR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/139,409
FILING DATE: 19-OCT-1993
ATTORNEY/AGENT INFORMATION:
NAME: Fitting, Thomas
REGISTRATION NUMBER: 34,163
REFERENCE/DOCKET NUMBER: TSI 332.3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 784-9399
TELEFAX: (619) 784-2937
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-591-632-24
Query Match 42.9%, Score 3, DB 4, Length 5:
Best Local Similarity 100.0%, Pred. No. 2e+05:
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0:
QY 4 YFT 6
DB 1 YFT 3
RESULT 15
US-09-109-879-42
Sequence 42, Application US/09109879
Patent No. 6274556
GENERAL INFORMATION:
APPLICANT: Schwender, Charles F.
APPLICANT: Shroff, Hitesh N.
TITLE OF INVENTION: INHIBITORS OF MADCAM-1-MEDIATED
CELL-CELL INTERACTIONS AND METHODS OF USE THEREOF
NUMBER OF SEQUENCES: 89
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Militia Drive
CITY: Lexington
STATE: Massachusetts
COUNTRY: USA
ZIP: 02421
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/109,879
FILING DATE: 02-JUL-1998
CLASSIFICATION: 514

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PRIOR APPLICATION DATA:
  APPLICATION NUMBER: PCT/US97/00291
  FILING DATE: 03-JAN-1997
PRIOR APPLICATION DATA: US 08/582,740
  APPLICATION NUMBER: US 08/582,740
  FILING DATE: 04-JAN-1996
  ATTORNEY/AGENT INFORMATION:
    NAME: BROOK, David E.
    REGISTRATION NUMBER: 22,592
  REFERENCE/DOCKET NUMBER: LKS95-12A2
  TELECOMMUNICATION INFORMATION:
    TELEPHONE: (781) 861-6240
    TELEFAX: (781) 861-9540
  INFORMATION FOR SEQ ID NO: 42:
    SEQUENCE CHARACTERISTICS:
      LENGTH: 5 amino acids
      TYPE: amino acid
      STRANDEDNESS:
      TOPOLOGY: linear
      MOLECULE TYPE: peptide
      FEATURE:
        NAME/KEY: Modified-site
        LOCATION: 1
        OTHER INFORMATION: /label= modified aa
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      FEATURE:
        NAME/KEY: Modified-site
        LOCATION: 5
        OTHER INFORMATION: /label= modified aa
        OTHER INFORMATION: /note= "Leucine - NH2"
US-09-109-879-42

Query Match      42.9%  Score 3;  DB 4;  Length 5;
Best Local Similarity 100.0%;  Pred. No. 2e-05;
Matches 4;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

QY  5 FTS 7
DB  2 FTS 4

Search completed: April 29, 2003, 08:55:04
Job time : 23.5833 secs

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DT 01-MAY-2000 (TREMBlrel. 13, Last annotation update)
 DE Putative IS90 transposase (Fragment).
 OS Escherichia coli.
 OC Bacteria; Proteobacteria; gamma subdivision: Enterobacteriaceae;
 OC Escherichia.
 OX NCBI_TaxID=562.
 RN [1]
 PP SEQUENCE FROM N.A.
 RC STRAIN=A295B;
 RX MEDLINE=99194747; PubMed=10094716;
 RA Rahn A., Drummel-Smith J., Whitfield C.
 RT "Conserved organization in the cps gene clusters for expression of
 Escherichia coli group 1 K antigens: relationship to the colicin *aciB*
 RT biosynthesis locus and the cps genes from *Klebsiella pneumoniae*."
 RL J. Bacteriol. 181:2307-2313(1999).
 DR EMBL: AF118251; AAD30008.1; -;
 FT NON_TER 8
 SQ SEQUENCE 8 AA; 1011 MW; F21DC1A3D1B41406 CRC64;

 Query Match 28.6%, Score 2; DB 2; Length 8;
 Best Local Similarity 100.0%; Pred. No. 6.7e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 QY 5 FT 6
 II
 Db 5 FT 6

 RESULT 7
 Q9R7T2
 ID Q9R7T2 PRELIMINARY; PRT; 8 AA.
 AC Q9R7T2;
 DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 13, Last annotation update)
 DE Hypothetical 1.0 kDa protein (Fragment).
 GN YQF3.
 OS Escherichia coli.
 OC Bacteria; Proteobacteria; gamma subdivision: Enterobacteriaceae;
 OC Escherichia.
 OX NCBI_TaxID=562;
 RN [1]
 PP SEQUENCE FROM N.A.
 RC STRAIN=K12;
 RX MEDLINE=97061202; PubMed=8905242;
 RA Oshima T., Aiba H., Baba T., Fujita K., Hayashi K., Honjo A.,
 RA Ikenoto K., Inada T., Itoh T., Kajihara M., Kawai K., Kashimoto K.,
 RA Kimura S., Kiradawa M., Makino K., Masuda S., Miki T., Mizobuchi K.,
 RA Mori H., Motomura K., Nakamura Y., Nishimura H., Nishio Y., Saito N.,
 RA Sempel G., Seki Y., Tadami H., Takemoto K., Wada C., Yamamoto Y.,
 RA Yano M., Horiuchi T.;
 RT "A 718-kb DNA Sequence of *Escherichia coli* K-12 Genome Corresponding
 RT to the 12,738,000-bp Region on the Linkage Map."
 RL DNA Res. 3:137-155(1996).
 DR EMBL: D90705; BAA35310.1; -;
 KW Hypothetical protein.
 FT NON_TER 1
 SQ SEQUENCE 8 AA; 914 MW; DF133B1D0C4B476A YQF64;

Query Match 28.6%, Score 2; DB 2; Length 8;
 Best Local Similarity 100.0%; Pred. No. 6.7e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KE 3
 II
 Db 7 KE 8

RESULT 8
 Q9R9E0
 ID Q9R9E0 PRELIMINARY; PRT; 8 AA.
 DT 01-MAY-2000 (TREMBlrel. 13, Created)

DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DT 01-MAY-2000 (TREMBlrel. 13, Last annotation update)
 DE Stage V sporulation protein E (Fragment).
 GN SPOVE.
 OS Bacillus subtilis.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;
 OC Bacillaceae; Bacillus.
 OX NCBI_TaxID=1423;
 RN [1]
 PP SEQUENCE FROM N.A.
 RC STRAIN=168;
 RX MEDLINE=91001529; PubMed=1391053;
 RA Henriques A.C., de Lencastre H., Piggot P.J.;
 RT "A *Bacillus subtilis* morphogene cluster that includes *spoVE* is
 RT involved in sporulation in a *spoVE* of *Escherichia coli*."
 RL Biochimie 74:735-748(1992).
 DR EMBL: X64258; CAA45556.1; -;
 FT NON_TER 8
 SQ SEQUENCE 8 AA; 893 MW; EE75A1A33421B1A6 CRC64;

Query Match 28.6%, Score 2; DB 2; Length 8;
 Best Local Similarity 100.0%; Pred. No. 6.7e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 IS 7
 II
 Db 6 IS 7

RESULT 9
 Q56759
 ID Q56759 PRELIMINARY; PRT; 8 AA.
 AC Q56759;
 DT 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE Halocacid dehalogenase (Fragment).
 GN DHLB.
 OS Xanthobacter autotrophicus.
 OC Bacteria; Proteobacteria; alpha subdivision: Rhizobiaceae group;
 OC Hyphomicrobium group; Xanthobacter.
 OX NCBI_TaxID=280;
 RN [1]
 PP SEQUENCE FROM N.A.
 RC STRAIN=GJ10; AND CV; MS0;
 RX MEDLINE=9517113; PubMed=7666610;
 RA Van der Ploeg J., Willemsen M., van Hall G., Janssen D.B.;
 RT "Adaptation of *Xanthobacter autotrophicus* GJ10 to trim-acetate due to
 RT activation and mobilization of the halocetate dehalogenase gene by
 RT insertion element IS1247."
 RL J. Bacteriol. 177:1348-1356(1995).
 DR EMBL: X84038; CAA58857.1; -;
 FT NON_TER 8
 SQ SEQUENCE 8 AA; 922 MW; F1A9C2D2D0D31056 CRC64;

Query Match 28.6%, Score 2; DB 2; Length 8;
 Best Local Similarity 100.0%; Pred. No. 6.7e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IK 2
 II
 Db 2 IK 3

RESULT 10
 P77556
 ID P77556 PRELIMINARY; PRT; 8 AA.
 AC P77556;
 DT 01-FEB-1997 (TREMBlrel. 02, Created)
 DT 01-FEB-1997 (TREMBlrel. 02, Last sequence update)
 DT 01-JAN-1999 (TREMBlrel. 09, Last annotation update)
 DE TRAY (Fragment).
 GN TRAY.

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OS Escherichia coli.
OG Plasmid IncFII F1.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ECOR11;
RC MEDLINE=96400908; PubMed=8807284;
FA Boyd E.F., Hill C.W., Rich S.M., Hartl D.L.
RT "Mosaic structure of plasmids from natural populations of Escherichia
KI coli.";
RL Genetics 143:1061-1100(1996).
DR EMBL: U50661; AAC44245.1; -
DR EMBL: U50650; AAC44234.1; -
DR EMBL: U50651; AAC44235.1; -
DR EMBL: U50652; AAC44236.1; -
DR EMBL: U50653; AAC44237.1; -
DR EMBL: U50654; AAC44238.1; -
DR EMBL: U50655; AAC44239.1; -
DR EMBL: U50656; AAC44240.1; -
DR EMBL: U50657; AAC44241.1; -
DR EMBL: U50658; AAC44242.1; -
DR EMBL: U50659; AAC44243.1; -
DR EMBL: U50660; AAC44244.1; -
KW Plasmid.
FT NON_TER 1 1
SQ SEQUENCE 8 AA: 834 MW: D335A5B0544735A1 CF 64:

Query Match 28.6%; Score 2; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 6.7e-05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 TS 7
DB 1 TS 2

RESULT 11
Q8RJ10 PRELIMINARY: PRT: 9 AA
AC Q8RJ10;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE DNA replication initiation protein (Fragment).
GN DNAA-LIKE.
OS Streptomyces caespitosus.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Streptomycineae; Streptomyces;
OX NCBI_TaxID=53502;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC27422.
FA Ma W., Mac X., Jie L., Qin Z.J., Jiang W.H., Guo P.S., Zhao G.P.
RT "Cloning, sequence analysis and function analysis of the replication
KI origin oriC of Streptomyces caespitosus ATCC27422."
RL Submitted (Apr-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: AJ458440; CAD30524.1; -
FT NON_TER 1 1
SQ SEQUENCE 8 AA: 915 MW: 04744535440451A7 CF 64:

Query Match 28.6%; Score 2; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 6.7e-05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IK 2
DB 5 IK 6

RESULT 12
P87225 PRELIMINARY: PRT: 8 AA
AC P87225;
DT 01-NOV-1996 (TrEMBLrel. 12, Created)
DT 01-NOV-1996 (TrEMBLrel. 12, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE GIN11 protein (Fragment).
GN GIN11 OR YLL065W.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RC Wedler H., Wedler E., Scharfe M., Wambutt R.
PL Submitted (May-1996) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA MIPS;
PI Submitted (May-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL: Z73189; CAA97518.2; -
DR SOD: S0003988; GIN11.
FT NON_TER 1 1
SQ SEQUENCE 9 AA: 1019 MW: 4F21A9C449D8B73P CF 64:

Query Match 28.6%; Score 2; DB 3; Length 8;
Best Local Similarity 100.0%; Pred. No. 6.7e-05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 FT 6
DB 6 FT 7

RESULT 13
Q9H4D3 PRELIMINARY: PRT: 8 AA
AC Q9H4D3;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE LIM domain only 1 protein (Fragment).
GN LMOL.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Blood;
FA Rueckmann T., Winterpacht A., Hankele T., Schmidt F.W., Patel B.V.
RT "Human PAC clone hPCP704K03781 (pM 781K3), sequenced in DHS Project.
KI (Comparative Sequencing of a 1 Mb Region in Man (Chromosome 11p15) and
RT Mouse (Chromosome 7))."
RL Submitted (Apr-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: A1277661; CAC14573.1; -
FT NON_TER 8 8
SQ SEQUENCE 9 AA: 930 MW: F4A133AA710596 CF 64:

Query Match 28.6%; Score 2; DB 4; Length 8;
Best Local Similarity 100.0%; Pred. No. 6.7e-05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KE 3
DB 6 KE 7

RESULT 14
Q15888 PRELIMINARY: PRT: 8 AA
AC Q15888;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)

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DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE (clone XP1588A) (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=PLACENTA;
 RA Lee C.-C., Yazdani A., Wehnert M., Bailey J., Couch L., Xiong M.,
 RA Coolbaugh M.I., Chinault C.A., Baldini A., Lindsay E.A., Zhao Z.-Y.,
 RA Caskey C.T.H.;
 RT "Isolation of chromosome-specific genes by reciprocal probing of
 RT arrayed cDNAs and cosmid libraries."
 RL Hum. Mol. Genet. 0:0-0(1995).
 DR EMRL: L32069; AAA73878.1; -;
 FT NON_TER 1 1
 FT NON_TER 8 8
 SQ SEQUENCE 8 AA: 1068 MW: 0315A37EAB5E0763 CR004;

 Query Match 28.6%; Score 2; DB 4; Length 8;
 Best Local Similarity 100.0%; Pred. No. 6.7e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 QY 3 EY 4
 DB 4 EY 4

 RESULT 15
 Q15893
 ID Q15893 PRELIMINARY; PRT; 8 AA.
 AC Q15893;
 DT 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE (clone XP587A) (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=PLACENTA;
 RA Lee C.-C., Yazdani A., Wehnert M., Bailey J., Couch L., Xiong M.,
 RA Coolbaugh M.I., Chinault C.A., Baldini A., Lindsay E.A., Zhao Z.-Y.,
 RA Caskey C.T.H.;
 RT "Isolation of chromosome-specific genes by reciprocal probing of
 RT arrayed cDNAs and cosmid libraries."
 RL Hum. Mol. Genet. 0:0-0(1995).
 DR EMRL: L32073; AAA73883.1; -;
 FT NON_TER 1 1
 FT NON_TER 8 8
 SQ SEQUENCE 8 AA: 874 MW: DAA1B6D7376456C5 CR004;

 Query Match 28.6%; Score 2; DB 4; Length 8;
 Best Local Similarity 100.0%; Pred. No. 6.7e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 QY 6 TS 7
 DB 7 TS 8

Search Completed: April 29, 2003, 08:53:23
 Job time : 29.4167 secs

GenCore version 5.1.4_p1_4578
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CM protein - protein search, using sw model

Run on: April 29, 2003, 08:30:44 ; Search time 16.3333 Seconds

(without alignments)
17.775 Million cell updates/sec

Title: US-09-647-749A-2

Perfect score: 7

Sequence: 1 KEYS ?

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 112992
segs: 41476329 residues

Word size :

Total number of hits satisfying chosen parameters: 246

Minimum PB seq length: 0

Minimum DB seq	length: 10
Maximum DB seq	length: 10

post-processing: Listing first 45 summaries

Database : swissprot_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query			ID	Description
	Score	Match	Length		
1	3	42/9	6	ASP2_LACSN	P02655 lactobacill
2	3	28/6	3	LIVE_VIBET	P03272 vibrio fisco
3	2	28/6	5	REP2_LITRO	P02072 litobacilli
4	2	28/6	5	REP2_LITRO	P02073 litobacilli
5	2	28/6	7	FAP2_ASCSU	P31890 ascaris rub
6	2	28/6	7	WAA3_ACHFP	P35921 achatina fu
7	2	28/6	8	ACI_THUAL	P18691 thomus alb
8	2	28/6	8	AKH_LIBAU	P35418 libellula a
9	2	28/6	8	AKH_TABAT	P14595 tabanus atr
10	2	28/6	8	HFE2_PERAM	P04549 periplaneta
11	2	28/6	8	LMP2_LOCOM	P32396 locusta mig
12	2	28/6	8	LFP_LEUMA	P13049 leucophaea
13	2	28/6	8	DMV_OEPL	P34555 ophiocent
14	2	28/6	9	QZAF_CAPRA	P35556 capreolus
15	2	28/6	9	QZAF_THOGE	P03977 thomomys
16	2	28/6	9	NEUM_CAVIP	P34965 cavia force
17	2	28/6	9	NEUX_HUMAN	P04277 homo sapien
18	2	28/6	9	OXYF_SCYCA	P42997 scyllorhinu
19	2	28/6	9	OXYF_OCTEP	P00029 octopus vul
20	2	28/6	9	OXYF_OCTEP	P40929 homo sapien
21	2	28/6	9	UHA2_HUMAN	P35825 atylocarte
22	2	28/6	10	CON1_CHEEP	P06677 chelyosoma
23	2	28/6	10	HFE1_ROMMI	P18110 romalea mic
24	2	28/6	10	HFE2_CARMO	P11385 carausius m
25	2	28/6	10	HFE2_TABAT	P14596 tabanus atr
26	2	28/6	10	LMP2_LOCOM	P41498 locusta mig
27	2	28/6	10	SVF_TAMIF	P44464 campylorh
28	2	28/6	10	UPA4_HUMAN	P30090 homo sapien
29	2	28/6	10	QZAF_THLTP	P38007 ethamydia
30	1	14/3	3	GRWU_HUMAN	P01157 homo sapien
31	1	14/3	4	ACHU1_ACHFU	P35904 achatina fu
32	1	14/3	4	QZMS_PSECH	P19918 pseudomonas
33	1	14/3	4	EOS1_HUMAN	P02731 homo sapien

ALIGNMENTS

RESIST 1

	ASTF2_LACSIN	STANDARD:	EFT:	6 AA.
ID	ASIF2_LACSN			
AD	P82655;			
DT	16-OCT-2001 (Rel 40, Created)			
ET	16-OCT-2001 (Rel 40, Last sequence update)			
LT	16-OCT-2001 (Rel 40, Last annotation update)			
DE	Acid shock protein 2 (Fragment).			
OR	Lactobacillus sanfranciscensis (Lactobacillus sanfrancisco).			
OC	Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;			
CC	Lactobacillus.			
OX	NCBI_TaxId=1625;			
RN	[1]			
RP	SEQUENCE.			
RC	STRAIN=CBL1			
EX	MEDLINE=27329712, PMID=11479463;			
FA	De Angelis M, Altini D, Pallini V, De Concellis F.S., Gibellini M.			
PL	"The acid-stress response in Lactobacillus sanfranciscensis CBL1".			
FL	Microbiology 147:1463-1474(2001).			
TI	INDUCTION, AVEREPRRESS IN ACID ENVIRONMENTS.			
NT	NON TER			
ET	SEQUENCE			
PT	CBL1			
SA	SANFRANCISCO (CBL1)			

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Query Match 42.9%; Score 3; DB 1; Length 6;
Res+ Local similarity 100.0%;
Prod NO. 1.10.05;
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KEYWORDS:

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RESULT 2

LINE	VIBRI	STANDARD	PRT:	AA
10	LUPE VIBRI			
11	1242727			
12	01-NAF 1992 (Feb. 21, Created)			
13	01-NAF 1992 (Feb. 21, Last sequence update)			
14	01-NAF 1996 (Feb. 24, Last annotation update)			
15	Long-chain-fatty-acid-luciferase-encoding gene (FC 2.1.13) (Aryl- protein synthase) (Fragment).			
16	LUPE			
17	GN			
18	LUPE			
19	GN			
20	Vibrio fischeri			
21	Ratified Fatty Acid Lactation gene synthesis. Vibrinacaeae Vibrin			
22	NCBI Taxid=668			
23	NCBI Taxid=668			
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100	NCBI Taxid=668			

FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 FT MOD_RES 8 8 AMIDATION.
 SU SEQUENCE 8 AA: 949 MW: 86786771A9D1A736 CRC64;
 Query Match 28.6%; Score 2; DB 1; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1.1e-05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 5 FT 6
 DB 4 FT 5
 RESULT 10
 HTF2_PERAM STANDARD: PRI: 8 AA.
 AC P04549;
 DT 13-AUG-1987 (Rel. 05, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 01-FEB-1994 (Rel. 28, Last annotation update)
 DE Hypertrichalosaemic factor II (Neuropeptide M II) (Periplaneta CC 2)
 DE (PeA-CAH-II) (LeD-CC-II) (Hypertrichalosaemic neuropeptide II).
 OS Periplaneta americana (American cockroach).
 OS Leptinotarsa decemlineata (Colorado potato beetle), and
 OS Blattella orientalis (Oriental cockroach).
 CC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
 CC Insecta; Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
 CC Blattodea; Blattellidae; Periplaneta.
 CC NCBI_TaxID=578; 7539; 6976;
 RN [1]
 RP SEQUENCE.
 RC SPECIES=P.americana;
 RX MEDLINE=8605559; PubMed=548628;
 RA Witten J.L., Schaffer M.H., O'Shea M., Cook J., Hemling M.E.,
 RA Riechart K.L., Jr.
 RA "Structures of two cockroach neuropeptides synthesized by fast atom
 RF bombardment mass spectrometry."
 RL Biochem. Biophys. Res. Commun. 124:350-356(1984).
 RN [2]
 RP SEQUENCE.
 RC SPECIES=P.americana;
 RX MEDLINE=84298179; PubMed=6571255;
 RA Scarborough R.M., Jamieson G.C., Kalish P., Warner S.J., McEnroe G.A.,
 RA Miller C.A., Schooley D.A.
 RA "Isolation and primary structure of two peptides with
 RF cardioacceleratory and hyperglycemic activity from the corpora
 RL cardaca of Periplaneta americana."
 RL Proc. Natl. Acad. Sci. U.S.A. 81:5575-5579(1984).
 RN [3]
 RP SEQUENCE.
 RC SPECIES=B.orientalis; TISSUE=Corpora cardaca;
 RX MEDLINE=90255650; PubMed=2340112;
 RA Gaede G., Pinehart K.L., Jr.
 RA "Primary structures of hypertrichalosaemic neuropeptides isolated from
 RF the corpora cardaca of the cockroaches Leucophaea maderae, and
 RF Chromaphorina porteri. Blattella germanica and Blattella orientalis
 RF and of the stick insect Extatosoma tiaratum assigned by tandem fast
 RF atom bombardment mass spectrometry."
 RL Biol. Chem. Hoppe-Seyler 371:345-354(1990).
 CC -1- FUNCTION: HYPERTRICHALOSAEMIC FACTORS ARE NEUROPEPTIDES THAT
 CC ELEVATE THE LEVEL OF TREHALOSE IN THE HEMOLYMPH (TREHALOSE IS
 CC THE MAJOR CARBOHYDRATE IN THE HEMOLYMPH OF INSECTS).
 CC -1- SIMILARITY: BELONGS TO THE AKH / HRTH / APCH FAMILY.
 DR PIP: A05170; A05170;
 PIP: S08496; S08496;

DR PIR: B44960; B44960.
 DR PIR: B49823; B49823.
 DR InterPro: IPR002047; AKH.
 DR PROSITE: PS00256; AKH; 1.
 KW Neuropeptide; Amidation.
 FT MOD_RES 1 1
 FT MOD_RES 8 8
 SU SEQUENCE 8 AA: 1006 MW: 86745771A9D1A736 CRC64;
 AMIDATION.

Query Match 28.6%; Score 2; DB 1; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1.1e-05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0;

QY 5 FT 6
 DB 4 FT 5

RESULT 11

LMT2_LOCM1 STANDARD: PRI: 8 AA.

ID LMT2_LOCM1

AC F22396;

DT 01-AUG-1991 (Rel. 19, Created)

DT 01-AUG-1991 (Rel. 19, Last sequence update)

DT 01-AUG-1991 (Rel. 19, Last annotation update)

DE Locustamyotropin 2 (LOM-MI-2).

OS Locusta migratoria (Migratory locust).

CC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;

CC Insecta; Pterygota; Neoptera; Orthopteroidea; Orthoptera; Caelifera;

CC Acridomorpha; Acridoidea; Acrididae; Caelipodinae; Locusta.

CC NCBI_TaxID=7004;

RN [1]

RP SEQUENCE.

RC TISSUE=Corpora cardaca;

RA Schoofs L., Holman G.M., Hayes T.K., Nachman R.J., de Leeuw A.J.

RA "Isolation, identification and synthesis of locustamyotropin II, an

RA additional neuropeptide of Locusta migratoria. Member of the

RA cephalomyotropic peptide family."

RL Insect Biochem. 20:479-484(1990).

CC -1- FUNCTION: MEDIATES VISCERAL MUSCLE CONTRACTILE ACTIVITY

CC (MYOTROPIC ACTIVITY).

CC -1- SIMILARITY: BELONGS TO THE PYROKININ FAMILY.

DE InterPro: IPR001484; PYROKININ.

DE PROSITE: PS00539; PYROKININ; 1.

KW Neuropeptide; Amidation; Pyrokinin.

FT MOD_RES 8 8

SU SEQUENCE 8 AA: 934 MW: 26341771A9CAA87B CRC64;

AMIDATION.

Query Match 28.6%; Score 2; DB 1; Length 8;

Best Local Similarity 100.0%; Pred. No. 1.1e-05;

Matches 2; Conservative 0; Mismatches 0; Indels 0;

QY 5 FT 6

DB 4 FT 5

RESULT 12

LPK_LEUMA

ID LPK_LEUMA

AC P13049;

DT 01-JAN-1990 (Rel. 13, Created)

DT 01-FEB-1994 (Rel. 28, Last sequence update)

DT 01-FEB-1994 (Rel. 28, Last annotation update)

DE Leukopyrokinin (LPK) (LEM-PK).

OS Leucophaea maderae (Madeira cockroach).

CC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;

CC Insecta; Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;

CC Blattodea; Blaberidae; Leucophaea.

CC NCBI_TaxID=6698;

RN [1]

RP SEQUENCE.

FX METLINE=8626041; PubMed=3015140;

RA Nachman R.J., Holman G.M., Cook B.J.:
 RT "Active fragments and analogs of the insect neuropeptide
 RT leucopyrokinin: structure-function studies."
 RL Biochem. Biophys. Res. Commun. 137:936-942(1986).
 RN (2).
 RP SEQUENCE, AND SYNTHESIS.
 RC TISSUE-Head;
 RA MEDLINE=8705251; PubMed=2877794;
 RX Holman G.M., Cook B.J., Nachman R.J.:
 RT "Primary structure and synthesis of a blocked neuropeptide
 RT neuropeptide isolated from the cockroach, *Nauphoeta cinerea*."
 RL Comp. Biochem. Physiol. 85C:219-224(1986).
 CC -1- FUNCTION: MEDIATES VISCERAL MUSCLE CONTRACTION LE ACTIVITY
 CC (MYOTROPIC ACTIVITY).
 CC -1- MISCELLANEOUS: AN ANALOG WITHOUT THE N-TERMINAL PCA RESIDUE WAS
 CC SYNTHESIZED AND FOUND TO EXHIBIT GREATER ACTIVITY (144%) THAN THE
 CC PARENT NEUROPEPTIDE. THE PORTION OF THE SEQUENCE OF LEK MOST
 CC CRITICAL FOR THE MYOTROPIC PROPERTIES IS LIMITED TO THE
 CC PENTAPEPTIDE FRAGMENT FTPLR.
 CC -1- SIMILARITY: BELONGS TO THE PYROKININ FAMILY
 CC PIR: A23967; A23957.
 DR InterPro: IPR001434; Pyrokinin.
 DR PROSITE: PS00549; PYROKININ; 1.
 KW Neuropeptide; Amidation; Pyrokinin
 FT MOD_RES 1 1 PYROGLUTAMINE CARBOXYLIC ACID.
 FT MOD_RES 8 8 AMIDATION.
 SQ SEQUENCE 8 AA: 949 MW: 92341771A9D5A1B6 CRG04;
 Query Match 29.6%, Score 2; DB 1; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1; Le-05; Indels 0;
 Matches 2; Conservative 0; Mismatches 0; Gaps 0;
 QY 6 TS 7
 DB 2 TS 3
 RESULT 13
 ID ORMY_ORC11 STANDARD: PRT: 8 AA.
 AC P82455;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Oremyotrofin (ORM)
 OS Oremyotrofin (ORM)
 CC Eukaryota, Metazoa, Arthropoda, Mandibulata, Pancrustacea, Crustacea,
 CC Eukaryota, Metazoa, Arthropoda, Mandibulata, Pancrustacea, Crustacea,
 CC Malacostraca, Eumalacostraca, Eucarida, Decapoda, Pleocyemata,
 CC Astacidea, Astacidea, Cambaridae, Decapoda, Pleocyemata,
 CC NCBI_TaxID=28179;
 RN (1)
 RP SEQUENCE, MASS SPECTROMETRY, AND AMIDATION.
 RC TISSUE-Hindgut,
 RX MEDLINE=20411310; PubMed=10952880;
 RA Dirksen H., Burdzik S., Saurer A., Keller R.:
 RT "Two prokinins and the novel octapeptide ormyotrofin in the hindgut
 RT of the crayfish *Oreochelone limosa* identified by similarity
 RT neuropeptides originating together in neurons of the terminal
 RT abdominal ganglion."
 RL J. Exp. Biol. 203:2607-2618(2000).
 CC -1- FUNCTION: MYOTROPIC PEPTIDE, ENHANCES BOTH THE FREQUENCY AND
 CC AMPLITUDE OF SPONTANEOUS HINDGUT CONTRACTIONS. IT IS SYNTHESIZED
 CC BY ABDOMINAL GANGLIONIC NEURONS.
 CC -1- MASS SPECTROMETRY: MW=904.8; METHOD=FAB.
 KW Amidation; Neuropeptide.
 FT MOD_RES 8 8 AMIDATION.
 SQ SEQUENCE 8 AA: 505 MW: 57086161A9C0DAA4 CRG04;
 Query Match 29.6%, Score 2; DB 1; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1; Le-05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 5 FT 6

DB 4 FT 5
 II
 RESULT 14
 ID CCAP_CARMA STANDARD: PRT: 9 AA.
 AC P38556;
 DT 01-OCT-1994 (Rel. 40, Created)
 DT 01-OCT-1994 (Rel. 40, Last sequence update)
 DT 01-OCT-1994 (Rel. 40, Last annotation update)
 DE Cardioactive peptide (CCAP).
 CC Cardioactive peptide (CCAP).
 CC Cardinus maenas (Common shore crab) (Green crab).
 CC Manduca sexta (Tobacco hawkmoth) (Tobacco hornworm).
 CC Tenebrio molitor (Yellow mealworm) and
 CC Spodoptera eridania (Southern armyworm).
 CC Eukaryota, Metazoa, Arthropoda, Mandibulata, Pancrustacea, Crustacea,
 CC Malacostraca, Eumalacostraca, Eucarida, Decapoda, Pleocyemata,
 CC Brachyura, Eubrachyura, Portunoidae, Portunidae, Carcinus.
 CC NCBI_TaxID=6759; 7130; 7067; 37547;
 RN (1)
 RP SEQUENCE.
 RC SPECIES=Cumacea; TISSUE=Pericardial organs;
 RA Stauder J., Hilbich C., Reutterer K., Keller R.:
 RT "Unusual cardioactive peptide (CCAP) from pericardial organs of the
 RT shore crab *Cardinus maenas*."
 RL Proc. Natl. Acad. Sci. U.S.A. 84:5795-5799(1987).
 RN (2)
 RP SEQUENCE.
 RC SPECIES=M. sexta;
 EX MEDLINE=33051143; PubMed=1125284;
 RA Cheung C.C., Loi P.K., Sylwester A.W., Lee T.D., Tublitz N.J.:
 RT "Primary structure of a cardioactive neuropeptide from the tobacco
 RT hawkmoth, *Manduca sexta*."
 RL FEBS Lett. 313:165-168(1992).
 RN (3)
 RP SEQUENCE.
 RC SPECIES=T. molitor, and S. eridania; TISSUE=Head;
 RX MEDLINE=94176032; PubMed=8129851;
 RA Furuya K., Iino S., Reynolds S.E., Ota R.B., Hackett M.:
 RA Schooley D.A.:
 RT "Isolation and identification of a cardioactive peptide from *Tenebrio*
 RT molitor and *Spodoptera eridania*."
 RL Biol. Chem. Hoppe-Seyler 274:1065-1074(1993).
 CC -1- FUNCTION: THE EFFECT OF CCAP IS BOTH INO- AND CHRONOTROPIC.
 CC -1- TISSUE SPECIFICITY: STORED IN PERICARDIAL ORGANS AND RELEASED
 CC INTO THE HEMOLYPH.
 CC PIR: A23929; A23964;
 DB PIR: 227223; 527234;
 KW Neuropeptide; Amidation.
 FT DISULFID 3 9
 FT MOD_RES 9 9 AMIDATION.
 SQ SEQUENCE 9 AA: 474 MW: 65861A9C0D04F04 CRG04;
 Query Match 29.6%, Score 2; DB 1; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1; Le-05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 5 FT 6
 DB 6 FT 7
 II
 RESULT 15
 ID COXE_THUCR STANDARD: PRT: 9 AA.
 AC P80975;
 DT 01-NOV-1997 (Rel. 45, Created)
 DT 01-NOV-1997 (Rel. 45, Last sequence update)
 DT 15-JUN-1998 (Rel. 46, Last annotation update)
 DE Cytochrome c oxidase polypeptide Via (CO 1.9.3.1) (Fragment).
 OS *Thunnus obesus* (Blueeye tuna).
 CC Eukaryota, Metazoa, Chordata, Clariata, Vertebrata, Euteleostomi;

CC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 CC Acanthomorpha; Acanthopterygii; Percormorpha; Perciformes; Scombroidei;
 CC Scombridae; Thunnus.
 QX NCBI_TaxID=8241;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Heart;
 FX MEDLINE=97454291 PubMed=9310366;
 RA Arnold S., Lee I., Kim M., Song E., Linder D., Gottspeich F.,
 RA Kadenbach B.;
 RT "The subunit structure of cytochrome-c oxidase from tuna heart and
 RT liver";
 RL Eur. J. Biochem. 248:99-103(1997).
 CC -!- FUNCTION: THIS PROTEIN IS ONE OF THE NUCLEAR-CODED POLYPEPTIDE
 CC CHAINS OF CYTOCHROME C OXIDASE, THE TERMINAL OXIDASE IN
 CC MITOCHONDRIAL ELECTRON TRANSPORT.
 CC -!- CATALYTIC ACTIVITY: 4 ferrocyclochrome c + (2) + 4 ferrocyclochrome
 CC c + 2 H(2)O.
 CC -!- SUBCELLULAR LOCATION: Mitochondrial inner membrane.
 CC -!- SIMILARITY: BELONGS TO THE CYTOCHROME C OXIDASE VIA FAMILY.
 DR InterPro: IPR001449; COX6A.
 DR PROSITE: PS01329; COX6A; PARTIAL.
 KW Oxidoreductase; Inner membrane; Mitochondrion.
 FT NON_TER 1 1
 FT NON_TER 9 9
 SQ SEQUENCE 9 AA: 1136 MW: 526072929077658 kDa64;

Query Match 28.6%; Score 2; DB 1; Length 9;
 Best Local Similarity 100.0%; Pred.No. 1.1e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KE 3
 Db 1 KE 2

Search completed: April 29, 2003, 08:52:29
 Job time : 17.3333 secs


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RESULT 4
B37325
pap/fmbrial regulatory protein papi - Escherichia coli (fragment)
C:Species: Escherichia coli
C:Date: 11-Sep-1992 #sequence_revision 11-Sep-1992 #text_change 23-Mar-1993
C:Accession: B37325
R: Braaten, B.A.; Blyn, L.B.; Skinner, B.S.; Low, P.A.
J. Bacteriol. 173, 1789-1800, 1991
A:Title: Evidence for a methylation-blocking factor (mbf) locus involved in pap pilus ex
A:Reference number: A37325; MUID:91154136; PMID:1071957
A:Accession: B37325
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-5 <BRA>
A:Cross-references: GB:M63747

Query Match 28.6% Score 2; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2 Re+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 YF 4
DB 3 YF 4

RESULT 4
PT0278
14 heavy chain C203 region (clone 4-68) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C:Accession: PT0278
R: Vanada, M.; Wasserman, P.; Feilichard, B.A.; Shiao, S.; Caton, A.J.; Faveira, G.
J. Exp. Med. 173, 395-407, 1991
A:Title: Preferential utilization of specific immunoglobulin heavy chain diversity and
A:Reference number: PT0222; MUID:91108337; PMID:1649102
A:Accession: PT0278
A:Molecule type: DNA
A:Residues: 1-5 <YAM>
A:Experimental source: B lymphocyte
C:Keywords: heterotrimer; immunoglobulin

Query Match 28.6% Score 2; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2 Re+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 YF 5
DB 1 YF 2

RESULT 5
PT0644
T-cell receptor beta chain V-D-1 region (111-13) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C:Accession: PT0644
R: Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A:Reference number: PT0509; MUID:91277601; PMID:1711558
A:Accession: PT0644
A:Status: translation not shown
A:Molecule type: mRNA
A:Residues: 1-5 <FEE>
A:Experimental source: newborn thymus, strain BALB.
C:Keywords: T-cell receptor

Query Match 28.6% Score 2; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2 Re+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 YF 6
DB 1 YF 6

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DB 4 YF 5

RESULT 6
H44817
34.5K structural protein - Leuconostoc oenos phase P32 (fragment)
C:Species: Leuconostoc oenos phase P32
C:Date: 31-Mar-1993 #sequence_revision 22-May-1998 #text_change 22-May-1998
C:Accession: H44817
R: Arendt, E.K.; Lonvaud, A.; Hammes, W.P.
J. Gen. Microbiol. 137, 2135-2139, 1991
A:Title: Lysogeny in Leuconostoc oenos.
A:Reference number: A44817; MUID 92085033; PMID:1748868
A:Accession: H44817
A:Molecule type: protein
A:Residues: 1-5 <ARE>
A:Note: sequence extracted from NRI backbone (NCRIP:70332)

Query Match 28.6% Score 2; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2 Re+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 TS 7
DB 3 TS 4

RESULT 7
F44817
34.5K structural protein - Leuconostoc oenos phase P54 (fragment)
C:Species: Leuconostoc oenos phase P54
C:Date: 31-Mar-1993 #sequence_revision 22-May-1998 #text_change 22-May-1998
C:Accession: F44817
R: Arendt, E.K.; Lonvaud, A.; Hammes, W.P.
J. Gen. Microbiol. 137, 2135-2139, 1991
A:Title: Lysogeny in Leuconostoc oenos.
A:Reference number: A44817; MUID:92085033; PMID:1748868
A:Accession: F44817
A:Molecule type: protein
A:Residues: 1-5 <ARE>
A:Note: sequence extracted from NRI backbone (NCRIP:70335)

Query Match 28.6% Score 2; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2 Re+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 TS 7
DB 3 TS 4

RESULT 8
B44817
34.5K structural protein - Leuconostoc oenos phase P211-15 (fragment)
C:Species: Leuconostoc oenos phase P211-15
C:Date: 31-Mar-1993 #sequence_revision 22-May-1998 #text_change 22-May-1998
C:Accession: B44817
R: Arendt, E.K.; Lonvaud, A.; Hammes, W.P.
J. Gen. Microbiol. 137, 2135-2139, 1991
A:Title: Lysogeny in Leuconostoc oenos.
A:Reference number: A44817; MUID 92085033; PMID 1748868
A:Accession: B44817
A:Molecule type: protein
A:Residues: 1-5 <ARE>
A:Note: sequence extracted from NRI backbone (NCRIP:70342)

Query Match 28.6% Score 2; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2 Re+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 TS 7
DB 3 TS 4

```

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Dt      4 TS 4

RESULT 4
D44817
35K structural protein - Leuconostoc oenos phage PA5-12 (fragment)
C:Species: Leuconostoc oenos phage PA5-12
C:Date: 31-Mar-1993 #sequence_revision 22-Mar-1993 #text_change 22-Mar-1993
C:Accession: D44817
R:Arendt, E.F.; Leonard, A.; Hammes, W.P.
J Gen Microbiol 137, 2135-2139, 1991
A:Title: Lysogeny in Leuconostoc oenos
A:Reference number: A44817, MUID:9229233, PMID:171968
A:Accession: D44817
A:Molecule type: protein
A:Residues: 1-5 <ARE>
A>Note: sequence extracted from NCBI backbone (NCBI:70340)

Query Match      28.6%  Score 2; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 TS 7
DB 4 TS 4

RESULT 10
S02617
alcohol dehydrogenase (EC 1.1.1.1) chi - horse (fragment)
C:Species: Equus caballus (domestic horse)
C:Date: 28-Feb-1990 #sequence_revision 29-Feb-1992 #text_change 31-Jan-1997
C:Accession: S02617
R:Fairwell, T.; Tolia, P.; Kaiser, P.; Holmquist, P.; Pares, X.; Vallee, B.L.; Jourdain
PERS Lett 222, 99-103, 1987
A:Title: Acetylated N-terminal structures of class III alcohol dehydrogenases. Differences
A:Reference number: S02617; MUID:88005160; PMID:366405
A:Accession: S02617
A:Molecule type: protein
A:Residues: 1-6 <FAI>
C:Superfamily: alcohol dehydrogenase; long-chain alcohol dehydrogenase homology
C:Keywords: alcohol metabolism; NAD, oxidoreductase..

Query Match      28.6%  Score 2; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IK 2
DB 5 IK 6

RESULT 11
A31263
dihydrofolate reductase (EC 1.5.1.3) / thymidylate synthase (EC 2.1.1.45) - Plasmodium f
C:Species: Plasmodium falciparum
C:Date: 29-Feb-1990 #sequence_revision 29-Feb-1990 #text_change 20-Mar-1997
C:Accession: A31263
R:Peterson, D.S.; Walliker, D.; Wellens, T.E.
Proc Natl Acad Sci U S A 85, 9114-9118, 1988
A:Title: Evidence that a point mutation in dihydrolate reductase (thymidylate synthase)
A:Reference number: A31217; MUID:89057885; PMID:3290149
A:Accession: A31263
A>Status: not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-6 <PET>
C:Keywords: methyltransferase; NADP; oxidoreductas.

Query Match      28.6%  Score 2; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 TS 7

Dt      4 TS 4

RESULT 12
S17976
glucose isomerase - Thermoplasma bacterium saccharolyticum (fragment)
C:Species: Thermoplasma bacterium saccharolyticum
C:Date: 12-Feb-1998 #sequence_revision 12-Feb-1998 #text_change 17-Apr-1998
C:Accession: S17976
R:Lee, C.; Zeikus, J.G.
Biochem J 273, 565-571, 1991
A:Title: Purification and characterization of the most stable glucose isomerase from clo
A:Reference number: S15119; MUID:91144536; PMID:1996956
A:Accession: S17976
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-7 <LEE>
A>Note: the sequence from page 568 is inconsistent with that from page 566 in saying
A>Note: the source is identified as Thermoplasma bacter strain P6A

Query Match      28.6%  Score 2; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 YF 5
DB 4 YF 5

RESULT 13
P00254
18K protein 5507 - rice (strain Nihonbare) (fragment)
C:Species: Oryza sativa (rice)
C:Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 23-Mar-1995
C:Accession: P00254
R:Tsugita, A.
submitted to JIPID, April 1993
A:Reference number: P00206
A:Accession: P00254
A:Molecule type: protein
A:Residues: 1-7 <TSO>
A:Experimental source: leaf, chloroplast, strain Nihonbare
A>Note: molecular weight 18K, pI 4.4

Query Match      28.6%  Score 2; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KE 3
DB 5 KE 6

RESULT 14
S33244
neuromodulatory peptide Wamide1, giant African snail
C:Species: Achatina fulica (giant African snail)
C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 24-Jul-1997
C:Accession: S33244
R:Minikata, H.; Ishii, T.; Muraoka, Y.; Kobayashi, M.; Nishida, E.
FEBS Lett 323, 104-108, 1993
A:Title: Wamide1, 2 and 3: novel neuromodulatory peptides isolated from giant snail
A:Reference number: S33244; MUID:93265912; PMID:8495720
A:Accession: S33244
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-7 <MIN>

Query Match      28.6%  Score 2; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 2 KE 3
 II
 Db 2 KE 3

RESULT 15

PC1316
 large granule L3 chain - horseshoe crab (Tachypileus tridentatus) (fragment)
 C:Species: Tachypileus tridentatus
 C:Date: 10-Mar-1994 #sequence_revision 10-Mar-1994 #text_change 07-May-1999
 C:Accession: PC1316
 R:Shigenaga, T.; Takayama, Y.; Kawasaki, S.; Seki, N.; Muta, T.; Tsch, Y.; Ito, A.; Iwa
 J. Biochem. 114, 307-316, 1993
 A:Title: Separation of large and small granules from horseshoe crab (Tachypileus tridentatus)
 A:Reference number: PC1309; MOLIP-94110249; PMID-828718
 A:Accession: PC1316
 A:Molecule type: protein
 A:Residues: 1-7 <SH1>
 C:Comment: This protein participates in immobilization of invading microbes.

Query Match 28.6%; Score 2; DB 2; length 7;
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 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 TS 7
 II
 Db 1 TS 2

Search completed: April 29, 2003, 08:54:19
 Job time : 30.1667 secs

GenCore version 5.1.4.p5.4578
Copyright (c) 1995 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 25, 2003, 09:30:19, Search size 58,9167, Sequois
(without alignments)
15,832 Million cell updates/sec

Title: US-09-647-749A-2

Perfect score: 7

Sequence: 1 IKEYFIS 7

Scoring table: colgo

Gapop 60.0, Gapext 60.0

Searched: 908476 seqs, 13425620 residues

Word size: 0

Total number of hits satisfying chosen parameters: 174064

Minimum DB seq length: 0

Maximum DB seq length: 10

Post-processing: Listing first 45 summaries

Database: A_Geneseq_101002:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	7	100.0	7	AA1966	Hiv-1 gp120 indyco
2	4	57.1	5	AA1967	PD2 motif sequence
3	4	57.1	5	AA1968	Glycophorin C C-te
4	4	57.1	5	AA1969	Glycophorin C C-te
5	4	57.1	6	AA1970	PD2 motif sequence
6	4	57.1	6	AA1971	Glycophorin C C-te
7	4	57.1	6	AA1972	Glycophorin C C-te
8	4	57.1	6	AA1973	PD2 motif sequence
9	4	57.1	7	AA1974	Glycophorin C C-te
10	4	57.1	7	AA1975	Glycophorin C C-te

11	4	57.1	8	22	AA1976	PD2 motif sequence
12	4	57.1	8	22	AA1977	Glycophorin C C-te
13	4	57.1	8	22	AA1978	Glycophorin C C-te
14	4	57.1	8	16	AA1979	Peptide fragment
15	4	57.1	9	17	AA1980	Antigenic peptide
16	4	57.1	9	20	AA1981	PD2 motif sequence
17	4	57.1	9	20	AA1982	Amino acid sequence
18	4	57.1	9	20	AA1983	HLA-A2 binding p33
19	4	57.1	9	21	AA1984	Proteinase cell
20	4	57.1	9	21	AA1985	PD2 motif sequence
21	4	57.1	9	22	AA1986	PD2 motif sequence
22	4	57.1	9	23	AA1987	PD2 motif sequence
23	4	57.1	9	23	AA1988	PD2 motif sequence
24	4	57.1	10	17	AA1989	PD2 motif sequence
25	4	57.1	10	21	AA1990	PD2 motif sequence
26	4	57.1	10	22	AA1991	PD2 motif sequence
27	4	57.1	10	22	AA1992	PD2 motif sequence
28	4	57.1	10	23	AA1993	PD2 motif sequence
29	4	57.1	10	23	AA1994	PD2 motif sequence
30	4	57.1	10	23	AA1995	PD2 motif sequence
31	4	57.1	10	23	AA1996	PD2 motif sequence
32	4	57.1	10	23	AA1997	PD2 motif sequence
33	4	57.1	10	23	AA1998	PD2 motif sequence
34	4	57.1	10	23	AA1999	PD2 motif sequence
35	3	42.9	4	21	AA1980	PD2 motif sequence
36	3	42.9	4	21	AA1981	PD2 motif sequence
37	3	42.9	4	22	AA1982	PD2 motif sequence
38	3	42.9	4	22	AA1983	PD2 motif sequence
39	3	42.9	4	22	AA1984	PD2 motif sequence
40	3	42.9	4	22	AA1985	PD2 motif sequence
41	3	42.9	4	22	AA1986	PD2 motif sequence
42	3	42.9	4	22	AA1987	PD2 motif sequence
43	3	42.9	4	22	AA1988	PD2 motif sequence
44	3	42.9	4	22	AA1989	PD2 motif sequence
45	3	42.9	4	22	AA1990	PD2 motif sequence

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PT New peptides useful for inhibiting human immunodeficiency virus type 1
 PT (HIV-1) gp120 induced neuronal cell death
 XX
 PS Claim 1: Page 11: 16pp; English.
 XX
 CC AAY49695 and AAY49696 represent peptides which inhibit HIV 1 gp120
 CC induced neuronal cell death. Pharmaceutical compositions containing the
 CC peptides are useful for treating symptoms caused by neuronal cell loss.
 CC such conditions especially associated with HIV infection include
 CC encephalopathies, neuropathies, memory loss, dementia, depression,
 CC psychosis and opportunistic infections. The peptides act as antagonists
 CC of gp120-mediated neurotoxicity and subsequent neuronal degeneration.
 CC This enables therapeutic treatment of HIV infection and other
 CC inflammatory neurological diseases, including multiple sclerosis,
 CC tropical spastic paraparesis and Alzheimer's disease.
 XX
 SQ Sequence 7 AA:
 Query Match 100.0%; Score 7; DB 20; Length 7;
 Best Local Similarity 100.0%; Pred No. 7.4e-5;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KEYFTS 7
 DQ I I I I I I I
 DB 1 KEYFTS 7
 RESULT 2
 AAB55781
 ID AAB55781 standard; Peptide: 5 AA.
 XX
 AC AAB55781:
 XX
 DT 07-MAR-2001 (first entry)
 DE PDZ motif sequence #12.
 DE Hematopoietic cell, PDZ, PL, autoimmune disease, inflammation,
 KW allergy; asthma; multiple sclerosis; cancer; infection.
 KW Synthetic.
 OS
 XX Homo sapiens.
 XX W0200069896-A2.
 XX
 PD 23-NOV-2000.
 XX
 PF 12-MAY-2000; 2000WS-US13161.
 XX
 PF 14-MAY-1999; 990S-0134114.
 PF 14-MAY-1999; 990S-0134117.
 PF 14-MAY-1999; 990S-0134118.
 PF 21-OCT-1999; 990S-0160460.
 PF 26-OCT-1999; 990S-0162498.
 PF 13-DEC-1999; 990S-0170453.
 PF 14-JAN-2000; 2000US-0174153.
 PF 14-FEB-2000; 2000US-0182296.
 PF 11-APR-2000; 2000US-0196460.
 PF 11-APR-2000; 2000US-0196527.
 XX
 PA (ARBO-) ARBOR VITA CORP.
 XX
 Lu PS:
 XX
 WPI: 2001-080245/09.
 XX
 PT Modulating a biological function of an endothelial cell or
 PT hematopoietic cell, useful for treating autoimmune diseases and
 PT infectious diseases, by administering an antagonist that inhibits
 PT binding between a PDZ protein and a PL protein.
 XX
 XX Disclosures: Page 87-94; 141pp; English.
 XX
 CC The present invention relates to a new method for modulating a

CC biological function of an endothelial cell or hematopoietic cell. The
 CC method involves introducing into a cell, an antagonist that inhibits
 CC binding between a PDZ protein and a PL protein. The inhibitor is used
 CC to treat a disease mediated by hematopoietic cells, e.g. autoimmune
 CC disease. It may also be used to prevent transplantation rejection of
 CC a solid organ transplant. The method may also be used in the treatment
 CC of inflammation, allergy, inflammatory bowel diseases, ulcerative
 CC colitis, ileitis, psoriasis, asthma, atopic dermatitis, autoimmune
 CC diseases (e.g. rheumatoid arthritis, multiple sclerosis,
 CC insulin-dependent diabetes, Hashimoto thyroiditis, osteoarthritis,
 CC graft rejection, transplantation rejection), atherosclerosis, cancer,
 CC infectious diseases, ischemia, vasculitis and Crohn's disease.
 XX
 SQ Sequence 5 AA:
 Query Match 57.1%; Score 4; DB 22; Length 5;
 Best Local Similarity 100.0%; Pred. No. 7.8e-05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 KEYF 5
 DQ I I I I I
 DB 1 KEYF 4
 RESULT 3
 AAB57613
 ID AAB57613 standard; Peptide: 5 AA.
 XX
 AC AAB57613:
 XX
 DT 12-MAR-2001 (first entry)
 DE Glycophorin C C-terminal core sequence #2.
 XX
 KW Endothelial cell; hematopoietic cell; PDZ domain protein;
 KW PL domain protein; leukocyte activation; T cell surface receptor;
 KW synapse formation; transmembrane neurotransmitter receptor;
 KW autoimmune disease; transplantation rejection; inflammation; allergy;
 KW inflammatory bowel disease; ulcerative colitis; ileitis; psoriasis;
 KW asthma; atopic dermatitis; atherosclerosis; cancer; infectious disease;
 KW ischemia; vasculitis; Crohn's disease.
 XX
 OS Homo sapiens.
 XX W0200069897 A2.
 XX
 PD 23-NOV-2000.
 XX
 PF 12-MAY-2000; 2000WS-US13166.
 XX
 PF 14-MAY-1999; 990S-0134114.
 PF 14-MAY-1999; 990S-0134117.
 PF 14-MAY-1999; 990S-0134118.
 PF 21-OCT-1999; 990S-0160460.
 PF 24-OCT-1999; 990S-0162498.
 PF 13-DEC-1999; 990S-0170453.
 PF 14-JAN-2000; 2000US-0176195.
 PF 14-FEB-2000; 2000US-0182296.
 PF 11-APR-2000; 2000US-0196460.
 PF 11-APR-2000; 2000US-0196527.
 XX
 PA (ARBO-) ARBOR VITA CORP.
 XX
 Lu PS:
 XX
 WPI: 2001-025003/03.
 XX
 PT New inhibitors of binding of a PDZ protein and PL protein for
 PT inhibiting T cell-mediated response by hematopoietic cells, or for
 PT treating diseases characterized by inflammatory and humoral immune
 PT responses, e.g. inflammation, cancer.
 XX
 XX Disclosures: Page 93, 139pp, English.

XX The present invention relates to a method for mediating a biological
CC function of an endothelial cell or haematopoietic cell, comprises
CC introducing into a cell an antagonist that inhibits binding between a
CC PDZ domain protein and a PL domain protein to result in inhibition of
CC leukocyte activation. The present sequence is a core sequence of a PL
CC domain protein (a T cell surface receptor). PDZ domains of proteins are
CC named after three prototypical proteins: PSD-95, Drosophila large disc
CC protein and Zonula Occludin-1 protein. PDZ domain proteins are involved
CC in synapse formation by organising transmembrane neurotransmitter
CC receptors through intracellular interactions. The inhibitors identified
CC by the present invention can be used to treat a disease mediated by
CC haematopoietic cells, e.g. autoimmune disease, inflammation, allergy
CC (e.g. drug allergies), inflammatory bowel disease, ulcerative colitis,
CC ileitis, psoriasis, respiratory allergic diseases (e.g. asthma), atopic
CC dermatitis, autoimmune diseases (e.g. rheumatoid arthritis, multiple
CC sclerosis, insulin-dependent diabetes, cancers), infectious diseases (e.g.
CC osteoarthritis), atherosclerosis, cancers, Hashimoto thyroiditis,
CC viral infection), ischaemia, vasculitis and Crohn's disease. The
CC inhibitors can also be used to prevent transplantation rejection of a
CC solid organ transplant.

XX Sequence 5 AA:
SQ

Query Match 57.1%; Score 4; DP 22; Length 5;
Best Local Similarity 100.0%; Pred. No. 7.8e-05;
Matches 4; Conservative 0; Mismatches 0; Gaps 0;

QY 2 KEYF 5
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DB 1 KEYF 4

RESULT 4
AAB558023
ID AAB558023 standard. Peptide: 5 AA.
XX AC AAB58023;
XX DT 12-MAR-2001 (first entry)
XX DE Glycophorin C C-terminal core sequence #2.
XX Fodderheial cell; haematopoietic cell; PDZ domain protein;
KW PL domain protein; leukocyte activation; T cell surface receptor;
KW synapse formation; transmembrane neurotransmitter receptor;
KW autoimmune disease; transplantation rejection. Inflammation; allergy;
KW inflammatory bowel disease; ulcerative colitis ileitis; psoriasis;
KW asthma; atopic dermatitis; atherosclerosis; cancer; infectious disease;
KW ischaemia; vasculitis; Crohn's disease.
XX OS Homo sapiens.
XX FN WC200006988 A2.
XX PD 23-NOV-2000.
XX PF 12-MAY-2000; 2000WO-US13205.
XX PR 14-MAY-1999; 99US-0134114.
XX PR 14-MAY-1999; 99US-0134117.
XX PR 14-MAY-1999; 99US-0134118.
XX PR 21-OCT-1999; 99US-0160860.
XX PR 29-OCT-1999; 99US-0162498.
XX PR 13-DEC-1999; 99US-0170453.
XX PR 14-JAN-2000; 2000US-0176195.
XX PR 14-FEB-2000; 2000US-0182296.
XX PR 11-APR-2000; 2000US-0195453.
XX PR 11-APR-2000; 2000US-0195525.
XX PA (ARBO-) ARBOR VITA CORP.
XX Lu PS;

XX WPL 2001-06-07/07.
XX CC
XX Modulating a biological function of a haematopoietic cell for treating
XX an allergic response, or diseases mediated by immune system cells,
XX comprises introducing into the cell a PDZ-PL interaction enhancer or
XX inhibitor -
XX Disclosure: Page 95; 143pp; English.
XX The present invention relates to a method for modulating a biological
XX function of an endothelial cell or haematopoietic cell, comprises
XX introducing into a cell an antagonist that inhibits binding between a
XX PDZ domain protein and a PL domain protein to result in inhibition of
XX leukocyte activation. The present sequence is a core sequence of a PL
XX domain protein (a T cell surface receptor). PDZ domains of proteins are
XX named after three prototypical proteins: PSD-95, Drosophila large disc
XX protein and Zonula Occludin-1 protein. PDZ domain proteins are involved
XX in synapse formation by organising transmembrane neurotransmitter
XX receptors through intracellular interactions. The inhibitors identified
XX by the present invention can be used to treat a disease mediated by
XX haematopoietic cells, e.g. autoimmune disease, inflammation, allergy
XX (e.g. drug allergies), inflammatory bowel diseases, ulcerative colitis,
XX ileitis, psoriasis, respiratory allergic diseases (e.g. asthma), atopic
XX dermatitis, autoimmune diseases (e.g. rheumatoid arthritis, multiple
XX sclerosis, insulin-dependent diabetes, cancers), infectious diseases (e.g.
XX osteoarthritis), atherosclerosis, cancers, Hashimoto thyroiditis,
XX viral infection), ischaemia, vasculitis and Crohn's disease. The
XX inhibitors can also be used to prevent transplantation rejection of a
XX solid organ transplant.

XX Sequence 5 AA:
SQ

Query Match 57.1%; Score 4; DP 22; Length 5;
Best Local Similarity 100.0%; Pred. No. 7.8e-05;
Matches 4; Conservative 0; Mismatches 0; Gaps 0;

QY 2 KEYF 5
||||
DB 1 KEYF 4

RESULT 5
AAB55782
ID AAB55782 standard. Peptide: 6 AA.
XX AC AAB55782;
XX DT 07-MAR-2001 (first entry)
XX DE PDZ motif sequence #13.
XX OS Synthetic.
XX FN WC200006989 A2.
XX PD 23-NOV-2000.
XX PF 12-MAY-2000; 2000WO-US13161.
XX PR 14-MAY-1999; 99US-0134114.
XX PR 14-MAY-1999; 99US-0134117.
XX PR 14-MAY-1999; 99US-0134118.
XX PR 21-OCT-1999; 99US-0160860.
XX PR 29-OCT-1999; 99US-0162498.
XX PR 13-DEC-1999; 99US-0170453.
XX PR 14-JAN-2000; 2000US-0176195.
XX PR 14-FEB-2000; 2000US-0182296.
XX PR 11-APR-2000; 2000US-0195460.
XX PR 11-APR-2000; 2000US-0195527.


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XX PA (ARBO-) ARBOR VITA CORP.
XX PI Lu PS:
XX PR WPI: 2001-080245/09.
XX DR
XX PT Modulating a biological function of an endothelial cell or
XX PT hematopoietic cell; useful for treating autoimmune diseases and
XX PT infectious diseases, by administering an antagonist that inhibits
XX PT binding between a PDZ protein and a PL protein.
XX PS Disclosure: Page 87-94; 141pp; English.
XX CC The present invention relates to a new method for modulating a
XX CC biological function of an endothelial cell or hematopoietic cell. The
XX CC method involves introducing into a cell an antagonist that inhibits
XX CC binding between a PDZ protein and a PL protein. The inhibitor is used
XX CC to treat a disease mediated by hematopoietic cells, e.g. autoimmune
XX CC disease. It may also be used to prevent transplantation rejection of
XX CC a solid organ transplant. The method may also be used in the treatment
XX CC of inflammation, allergy, inflammatory bowel diseases, ulcerative
XX CC colitis, ileitis, psoriasis, asthma, atopic dermatitis, autoimmune
XX CC diseases (e.g. rheumatoid arthritis, multiple sclerosis,
XX CC insulin-dependent diabetes, Hashimoto thyroiditis, osteoarthritis,
XX CC graft rejection, transplantation rejection), atherosclerosis, cancer,
XX CC infectious diseases, ischemia, vasculitis and Crohn's disease.
XX SQ Sequence 6 AA:
Query Match 57.1%; Score 4; DB 22; Length 6;
Best Local Similarity 100.0%; Pred. No. 7.8e-05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 KEYF 5
DB 1111
2 KEYF 5
RESULT 6
AAB57614
ID AAB57614 standard; Peptide: 6 AA.
AC AAB57614;
XX 12-MAR-2001 (first entry)
XX Glycophorin C C-terminal core sequence #3.
XX Endothelial cell; hematopoietic cell; PDZ domain protein;
XX PL domain protein; leukocyte activation; T cell surface receptor;
XX synapse formation; transmembrane neurotransmitter receptor;
XX autoimmune disease; transplantation rejection; inflammation; allergy;
XX inflammatory bowel disease; ulcerative colitis; ileitis; psoriasis;
XX asthma; atopic dermatitis; atherosclerosis; cancer; infectious disease;
XX ischaemia; vasculitis; Crohn's disease.
XX Homo sapiens.
XX WO200069897-A2.
XX 23-NOV-2000.
XX 12-MAY-2000; 2000WO-US13156.
XX 14-MAY-1999; 99US-0134114.
XX 14-MAY-1999; 99US-0134117.
XX 21-OCT-1999; 99US-0134118.
XX 29-OCT-1999; 99US-0160869.
XX 13-DEC-1999; 99US-0162498.
XX 14-JAN-2000; 2000US-0170453.
XX 14-FEB-2003; 2000US-0162295.
PR 11-APR-2000; 2000US-0196460.
PR 11-APR-2000; 2000US-0196527.
XX PA (ARBO-) ARBOR VITA CORP.
XX PI Lu PS:
XX PR WPI: 2001-025003/03.
XX DR
XX PT New inhibitors of binding of a PDZ protein and PL protein for
XX PT inhibiting T cell-mediated response by hematopoietic cells, or for
XX PT treating diseases characterized by inflammatory and humoral immune
XX PT responses, e.g. inflammation, cancer.
XX PS Disclosure: Page 93; 135pp; English.
XX CC The present invention relates to a method for modulating a biological
XX CC function of an endothelial cell or hematopoietic cell, comprises
XX CC introducing into a cell an antagonist that inhibits binding between a
XX CC PDZ domain protein and a PL domain protein to result in inhibition of
XX CC leukocyte activation. The present sequence is a core sequence of a PL
XX CC domain protein (a T cell surface receptor). PDZ domains of proteins are
XX CC named after three prototypical proteins: PSD95, Drosophila large disc
XX CC protein and Shc1a. Occludin 1 protein, PDZ domain proteins are involved
XX CC in synapse formation by organising transmembrane neurotransmitter
XX CC receptors through intracellular interactions. The inhibitors identified
XX CC by the present invention can be used to treat a disease mediated by
XX CC hematopoietic cells, e.g. autoimmune disease, inflammation, allergy
XX CC (e.g. drug allergies), inflammatory bowel diseases, ulcerative colitis,
XX CC ileitis, psoriasis, respiratory allergic diseases (e.g. asthma), atopic
XX CC dermatitis, autoimmune diseases (e.g. rheumatoid arthritis, multiple
XX CC sclerosis, insulin-dependent diabetes, Hashimoto thyroiditis,
XX CC osteoarthritis), atherosclerosis, cancer, infectious diseases (e.g.
XX CC viral infection), ischaemia, vasculitis and Crohn's disease. The
XX CC inhibitors can also be used to prevent transplantation rejection of a
XX CC solid organ transplant.
XX SQ Sequence 6 AA:
Query Match 57.1%; Score 4; DB 22; Length 6;
Best Local Similarity 100.0%; Pred. No. 7.8e-05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 KEYF 5
DB 1111
2 KEYF 5
RESULT 7
AAB58024
ID AAB58024 standard; Peptide: 6 AA.
AC AAB58024;
XX 12-MAR-2001 (first entry)
XX Glycophorin C C-terminal core sequence #3.
XX Endothelial cell; hematopoietic cell; PDZ domain protein;
XX PL domain protein; leukocyte activation; T cell surface receptor;
XX synapse formation; transmembrane neurotransmitter receptor;
XX autoimmune disease; transplantation rejection; inflammation; allergy;
XX inflammatory bowel disease; ulcerative colitis; ileitis; psoriasis;
XX asthma; atopic dermatitis; atherosclerosis; cancer; infectious disease;
XX ischaemia; vasculitis; Crohn's disease.
XX Homo sapiens.
XX WO200069899-A2.
XX 23-NOV-2000.
XX 12-MAY-2000; 2000WO-US13295.

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XX PR 14-MAY-1999; 99US-0134114.
XX PR 14-MAY-1999; 99US-0134117.
XX PR 14-MAY-1999; 99US-0134118.
XX PR 21-OCT-1999; 99US-0160860.
XX PR 29-OCT-1999; 99US-0162498.
XX PR 13-DEC-1999; 99US-0170453.
XX PR 14-JAN-2000; 2000US-0182296.
XX PR 14-FEB-2000; 2000US-0182296.
XX PR 11-APR-2000; 2000US-0196460.
XX PR 11-APR-2000; 2000US-0196527.
XX PA (ARBO-) ARBOE VITA CORP.
XX PI Lu PS.
XX DR WPI: 2001-061214/07.
XX PT Modulating a biological function of a hematopoietic cell for treating
XX PT an allergic response, or diseases mediated by immune system cells,
XX PT comprises introducing into the cell a PDZ domain protein and a PL
XX PT inhibitor.
XX PS Disclosure: Page 96; 143pp; English.
XX CC The present invention relates to a method for modulating a biological
XX CC function of an endothelial cell or hematopoietic cell, comprises
XX CC introducing into a cell an antagonist that inhibits binding between a
XX CC PDZ domain protein and a PL domain protein to result in inhibition of
XX CC leukocyte activation. The present sequence is a core sequence of a PL
XX CC domain protein (a T cell surface receptor). PDZ domains of proteins at-
XX CC named after three prototypical proteins: PSD-95, Drosophila large disc
XX CC protein and Zonula Occludin 1 protein. PDZ domain proteins are involved
XX CC in synapse formation by organising transmembrane neurotransmitter
XX CC receptors through intracellular interactions. The inhibitors identified
XX CC by the present invention can be used to treat a disease mediated by
XX CC hematopoietic cells, e.g. autoimmune disease, inflammation, allergy
XX CC (e.g. drug allergies), inflammatory bowel diseases, ulcerative colitis,
XX CC ileitis, psoriasis, respiratory allergic diseases (e.g. asthma), atopic
XX CC dermatitis, autoimmune diseases (e.g. rheumatoid arthritis, multiple
XX CC sclerosis, insulin-dependent diabetes, Hashimoto thyroiditis,
XX CC osteoarthritis), atherosclerosis, cancers, infectious diseases (e.g.
XX CC viral infection), ischaemia, vasculitis and Crohn's disease. The
XX CC inhibitors can also be used to prevent transplantation rejection of a
XX CC solid organ transplant.
XX SQ Sequence 6 AA:
Query Match 57.1%, Score 4; DB 22; Length 6;
Best Local Similarity 100.0%; Pred. No. 7.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 KEYF 5
DB 1111
RESULT 8
AAB55783
ID AAB55783 standard; Peptide: 7 AA.
XX AC AAB55783;
XX DT 07-MAR-2001 (first entry)
XX DE PDZ motif sequence #14.
XX KW Hematopoietic cell; PDZ; PL: autoimmune disease; inflammation;
XX KW allergy; asthma; multiple sclerosis; cancer; infection.
XX OS Synthetic.
XX PN W020009896-A2.

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XX PU 23-NOV-2000.
XX PF 12-MAY-2000; 2000US-013161.
XX PP 14-MAY-1999; 99US-0134114.
XX PP 14-MAY-1999; 99US-0134117.
XX PP 14-MAY-1999; 99US-0134118.
XX PP 21-OCT-1999; 99US-0160860.
XX PP 29-OCT-1999; 99US-0162498.
XX PP 13-DEC-1999; 99US-0170453.
XX PP 14-JAN-2000; 2000US-0182296.
XX PP 14-FEB-2000; 2000US-0182296.
XX PP 11-APR-2000; 2000US-0196460.
XX PP 11-APR-2000; 2000US-0196527.
XX PA (ARBO-) ARBOE VITA CORP.
XX PI Lu PS.
XX DR WPI: 2001-061214/09.
XX PT Modulating a biological function of an endothelial cell or
XX PT hematopoietic cell, useful for treating autoimmune diseases and
XX PT infectious diseases, by administering an antagonist that inhibits
XX PT binding between a PDZ protein and a PL protein.
XX PS Disclosure: Page 87-94; 141pp; English.
XX CC The present invention relates to a new method for modulating a
XX CC biological function of an endothelial cell or hematopoietic cell. The
XX CC method involves introducing into a cell, an antagonist that inhibits
XX CC binding between a PDZ protein and a PL protein. The inhibitor is used
XX CC to treat a disease mediated by hematopoietic cells, e.g. autoimmune
XX CC disease. It may also be used to prevent transplantation rejection of
XX CC a solid organ transplant. The method may also be used in the treatment
XX CC of inflammation, allergy, inflammatory bowel diseases, ulcerative
XX CC colitis, ileitis, psoriasis, asthma, atopic dermatitis, autoimmune
XX CC diseases (e.g. rheumatoid arthritis, multiple sclerosis,
XX CC insulin-dependent diabetes, Hashimoto thyroiditis, osteoarthritis,
XX CC graft rejection, transplantation rejection), atherosclerosis, cancers,
XX CC infectious diseases, ischemia, vasculitis and Crohn's disease.
XX SQ Sequence 7 AA:
Query Match 57.1%, Score 4; DB 22; Length 7;
Best Local Similarity 100.0%; Pred. No. 7.8e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 KEYF 5
DB 1111
RESULT 9
AAB57615
ID AAB57615 standard; Peptide: 7 AA.
XX AC AAB57615;
XX DT 12-MAR-2001 (first entry)
XX DE Glycophorin C C-terminal core sequence #4.
XX KW Endothelial cell; hematopoietic cell; PDZ domain protein;
XX KW PL domain protein; leukocyte activation; T cell surface receptor;
XX KW synapse formation; transmembrane neurotransmitter receptor;
XX KW autoimmune disease; transplantation rejection; inflammation; allergy;
XX KW inflammatory bowel disease; ulcerative colitis; ileitis; psoriasis;
XX KW asthma; atopic dermatitis; atherosclerosis; cancer; infectious disease;
XX KW ischaemia; vasculitis; Crohn's disease.
XX PN Homo sapiens.

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XX KW W0200069848-A2
 XX
 XX
 PD 23-NOV-2000.
 XX PF 12-MAY-2000; 2000WS-0134114
 XX PR 14-MAY-1999; 940S-0134114.
 PR 14-MAY-1999; 940S-0134117.
 PR 14-MAY-1999; 940S-0134118.
 PR 21-OCT-1999; 940S-0160860.
 PR 13-DEC-1999; 940S-0170453.
 PR 14-JAN-2000; 2000WS-0176195.
 PR 14-FEB-2000; 2000WS-0182296.
 PR 11-APR-2000; 2000WS-0194460.
 PR 11-APR-2000; 2000WS-0196527.
 XX (ARBO-) ARBOR VITA CORP.
 XX Lu PS:
 XX WPI: 2001-025003403.
 XX
 PD New inhibitors of binding of a PLZ protein and PLZ protein for
 PT inhibiting T cell-mediated response by hematopoietic cells, or for
 PT treating diseases characterized by inflammatory and humoral immune
 PT responses, e.g. inflammation, cancer.
 XX
 XX Disclosure: Page 93; 139pp; English.
 XX
 CC The present invention relates to a method for modulating a biological
 CC function of an endothelial cell or hematopoietic cell, comprises
 CC introducing into a cell an antagonist that inhibits binding between a
 CC PDZ domain protein and a PL domain protein to result in inhibition of
 CC leukocyte activation. The present sequence is a core sequence of a PL
 CC domain protein (a T cell surface receptor). PDZ domains of proteins are
 CC named after three prototypical proteins: PSD95, Prosophila large disc
 CC protein and zonula occludin 1 protein. PDZ domain proteins are involved
 CC in synapse formation by organising transmembrane neurotransmitter
 CC receptors through intracellular interactions. The inhibitors identified
 CC by the present invention can be used to treat a disease mediated by
 CC hematopoietic cells, e.g. autoimmune disease, inflammatory diseases (e.g.
 CC (e.g. drug allergies), inflammatory bowel diseases, ulcerative colitis,
 CC dermatitis, psoriasis, respiratory allergic diseases (e.g. asthma), atopic
 CC osteoarthritis), atherosclerosis, cancers, infectious diseases (e.g.
 CC viral infection), ischaemia, vasculitis and Crohn's disease. The
 CC inhibitors can also be used to prevent transplantation rejection of a
 CC solid organ transplant.
 XX
 SQ Sequence 7 AA.
 Query Match 57.1%, Score 4; DP 22; Length 7;
 Best Local Similarity 100.0%; Pred. No. 7 Re+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 KEYS 5
 DB 3 KEYS 6
 RESULT 10
 AAB58025
 ID AAB58025 standard; Peptide: 7 AA.
 XX
 AC AAB58025;
 XX
 DT 12-MAR-2001 (first entry)
 XX
 DE Glycophorin C C-terminal core sequence #4.
 XX

KW Endothelial cell, hematopoietic cells; PDZ domain protein;
 KW PL domain protein; leukocyte activation; T cell surface receptor;
 KW synapse formation; transmembrane neurotransmitter receptor;
 KW autoimmune disease; transplantation rejection; inflammation; allergy;
 KW inflammatory bowel disease; ulcerative colitis; ileitis; psoriasis;
 KW asthma; atopic dermatitis; atherosclerosis; cancers; infectious diseases;
 KW ischaemia; vasculitis; Crohn's disease.
 OS Homo sapiens.
 XX
 XX W0200069848-A2.
 XX PD 23-NOV-2000.
 XX PF 12-MAY-2000; 2000WS-0134114.
 XX PR 14-MAY-1999; 940S-0134114.
 PR 14-MAY-1999; 940S-0134117.
 PR 14-MAY-1999; 940S-0134118.
 PR 21-OCT-1999; 940S-0160860.
 PR 13-DEC-1999; 940S-0170453.
 PR 14-FEB-2000; 2000WS-0176195.
 PR 14-FEB-2000; 2000WS-0182296.
 PR 11-APR-2000; 2000WS-0194460.
 PR 11-APR-2000; 2000WS-0196527.
 XX (ARBO-) ARBOR VITA CORP.
 XX Lu PS:
 XX WPI: 2001-025003403.
 XX
 PD Modulating a biological function of a hematopoietic cell for treating
 PT an allergic response, or diseases mediated by immune system cells,
 PT comprises introducing into the cell a PDZ-PL interaction enhancer or
 PT inhibitor.
 XX
 XX Disclosure: Page 96; 143pp; English.
 XX
 CC The present invention relates to a method for modulating a biological
 CC function of an endothelial cell or hematopoietic cell, comprises
 CC introducing into a cell an antagonist that inhibits binding between a
 CC PDZ domain protein and a PL domain protein to result in inhibition of
 CC leukocyte activation. The present sequence is a core sequence of a PL
 CC domain protein (a T cell surface receptor). PDZ domains of proteins are
 CC named after three prototypical proteins: PSD95, Prosophila large disc
 CC protein and zonula occludin 1 protein. PDZ domain proteins are involved
 CC in synapse formation by organising transmembrane neurotransmitter
 CC receptors through intracellular interactions. The inhibitors identified
 CC by the present invention can be used to treat a disease mediated by
 CC hematopoietic cells, e.g. autoimmune disease, inflammatory diseases (e.g.
 CC (e.g. drug allergies), inflammatory bowel diseases, ulcerative colitis,
 CC dermatitis, psoriasis, respiratory allergic diseases (e.g. asthma), atopic
 CC osteoarthritis), atherosclerosis, cancers, infectious diseases (e.g.
 CC viral infection), ischaemia, vasculitis and Crohn's disease. The
 CC inhibitors can also be used to prevent transplantation rejection of a
 CC solid organ transplant.
 XX
 SQ Sequence 7 AA;
 Query Match 57.1%, Score 4; DP 22; Length 7;
 Best Local Similarity 100.0%; Pred. No. 7 Re+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 KEYS 5
 DB 3 KEYS 6
 RESULT 11

QY 2 KEVF 5
DB 4 KEVF 7

RESULT 13

AAB58026
ID AAB58026 standard; Peptide: 9 AA.

AC AAB58026;

XX 12-MAR-2001 (first entry)

DE Glycophorin C C-terminal core sequence #5.

XX Endothelial cell, haematopoietic cell, P22 domain protein.
KW PL domain protein; leukocyte activation; T cell surface receptor;
KW synapse formation; transmembrane neurotransmitter receptor;
KW autoimmune disease; transplantation rejection; inflammation; allergy;
KW inflammatory bowel disease; ulcerative colitis; ileitis; psoriasis;
KW asthma; atopic dermatitis; atherosclerosis; cancer; infectious disease;
KW ischaemia; vasculitis; Crohn's disease.

XX Homo sapiens.

XX W0200069898-A2.

XX 23-NOV-2000.

XX 12-MAY-2000; 2000WO-US13205.

XX 14-MAY-1999; 99US-0134114.

XX 14-MAY-1999; 99US-0134117.

XX 14-MAY-1999; 99US-0134118.

XX 21-OCT-1999; 99US-0160860.

XX 29-OCT-1999; 99US-0162498.

XX 13-DEC-1999; 99US-0170453.

XX 14-JAN-2000; 2000US-0176195.

XX 14-FEB-2000; 2000US-0182296.

XX 11-APR-2000; 2000US-0194460.

XX 11-APR-2000; 2000US-0195527.

XX (ARBOR) ARBOR VITA CORP.

XX Lu PS;

XX WPI: 2001-04-1214/07

XX Modulating a biological function of a hematopoietic cell for treating
PT an allergic response, or diseases mediated by immune system cells,
PT comprises introducing into the cell a PD2-PL interaction enhancer or
PT inhibitor.

XX Disclosure: Page 96; 143pp; English.

XX The present invention relates to a method for modulating a biological
CC function of an endothelial cell or hematopoietic cell, comprises
CC introducing into a cell an antagonist that inhibits binding between a
CC P22 domain protein and a PL domain protein to result in inhibition of
CC leukocyte activation. The present invention is a core sequence of a PL
CC domain protein (a T cell surface receptor). P22 domains of proteins are
CC named after three prototypical proteins: p22^L, p22^H, p22^S. p22^L is a
CC protein and p22^H and p22^S are proteins. P22 domain proteins are involved
CC in synapse formation by organising transmembrane neurotransmitter
CC receptors through intracellular interactions. The inhibitors identified
CC by the present invention can be used to treat a disease mediated by
CC haematopoietic cells, e.g. autoimmune disease, inflammation, allergy
CC (e.g. drug allergies), inflammatory bowel diseases, ulcerative colitis,
CC ileitis, psoriasis, respiratory allergic diseases (e.g. asthma), atopic
CC dermatitis, autoimmune diseases (e.g. rheumatoid arthritis, multiple
CC sclerosis, insulin-dependent diabetes, Hashimoto thyroiditis, Crohn's
CC osteoarthritis), atherosclerosis, cancers, infectious diseases (e.g.
CC viral infection), ischaemia, vasculitis and Crohn's disease. The

CC inhibitors can also be used to prevent transplantation rejection of a
CC solid organ transplant.

SQ Sequence 8 AA:

Query Match 57.1%; Score 4; DB 22; Length 8;
Best Local Similarity 100.0%; Pred. No. 7.8e-05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KEVF 5

DB 4 KEVF 7

RESULT 14

AAR59225
ID AAR59225 standard; peptide: 9 AA.

XX AAR59225;

XX AAR59225;

XX 04-MAY-1995 (first entry)

XX Peptide fragment (1.0268) of p53 binds HLA-A2.1.

XX antigen; epitope; immunogenic target protein; PSA; HBVc; HBVs; ERV;
KW HIV1; core antigen; surface antigen; pharmaceutical composition;
KW in vivo; ex vivo; therapeutic; diagnostic; MHC class I molecule;
KW major histocompatibility complex; HLA-A2.1; 9mer; 10mer; epitope;
KW human leukocyte antigen.

XX Homo sapiens.

XX W09420127-A.

XX 15-SEP-1994.

XX 04-MAR-1994; 94WO-US02353.

XX 04-MAY-1994; 94US-0027146.

XX 04-NOV-1994; 94US-0073205.

XX 24-NOV-1994; 94US-0159184.

XX (CYTE-) CYTEL CORP.

XX Grey HM, Kast WM, Settle A, Sidney J;

XX WPI: 1994-102679/37.

XX Immunogenic peptide(s) having an HLA-A2.1 binding motif - used
PT for treatment of phytoaxis of cancer; virus infection or
PT autoimmune diseases.

XX Example 5; Page 105; 138pp; English.

XX AAR59104-264 are immunogenic 9mer peptides that contain a HLA-A2.1
CC binding motif. These peptides bind HLA-A2.1 and have a binding affinity
CC of at least 14 as compared to a reference peptide (AAR71293). AAR59225
CC has an IC50 of 0 and the sequence occurs at position 322 in the p53
CC protein. The peptides of the invention can induce cytotoxic T lymphocytes
CC which can react with target cells. They can be used for the treatment of
CC phytoaxis of cancer, e.g. prostate cancer or lymphoma, etc.

SQ Sequence 9 AA:

Query Match 57.1%; Score 4; DB 15; Length 9;
Best Local Similarity 100.0%; Pred. No. 7.8e-05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 EYFT 6

DB 5 EYFT 8

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RESULT 15
AAR97542
ID AAR97542 standard; peptide; 9 AA.
XX
AC AAR97542;
XX
DT 12-FEB-1997 (first entry)
XX
DE Antigenic peptide, corresp to p53 aa 322-330.
XX
FW p53; Her-2; Neu; aa; amino acid; CTL; cytotoxic T lymphocyte; target;
KW malignant cell; antigenic; vaccine; immunisation; activation.
XX
OS Homo sapiens.
XX
PN WO9618409-A1.
XX
PD 20-JUN-1996.
XX
PF 14-DEC-1995; 95WO-0516415
XX
PR 14-DEC-1994; 94US-0355558.
XX
PA (SCRI ) SCRIPPS RES INST.
XX
PI Sherman LA;
XX
WPI: 1996-300385/30.
XX
PT In vivo activation of tumour-specific cytotoxic T lymphocytes - by
PT contacting with polypeptide(s) derived from human p53 or Her-2/Neu
PT proteins
XX
PS Example 4; Page 94; 158pp; English.
XX
CC AAR97517-P097544 are antigenic p53-derived peptides synthesised to be
CC used in an assay for identifying peptides capable of activating
CC cytotoxic T lymphocytes (CTLs) which specifically target malignant
CC cells. CTL-activating peptides can be used in a vaccine for
CC protecting against tumour cell formation. CTLs activated by the
CC peptides will lyse tumour cells displaying specific peptides.
CC Antibodies against CTL-activating peptides are useful for the
CC identification of other similar compounds which may be useful for
CC treating cancer or virally-infected cells, or for diagnosis. The
CC peptide and vaccines produced provide immunity to a high percentage
CC of different ethnic groups, i.e. those with different HLA alleles.
XX
SQ Sequence 9 AA:

Query Match 57.1%; Score 4; DB 17; Length 9;
Best Local Similarity 100.0%; Pred. No. 7.9e-05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 EYFT 6
Db 5 EYFT 8

Search completed: April 29, 2003, 08:51:54
Job time : 59.9167 secs

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